

SEQUENZPROTOKOLL

<110> BASF Aktiengesellschaft

<120> MetF

<130> M/43126

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<210> .1

<211> 984

<212> DNA

<213> corynebacterium diphtheriae

<220>

<221> CDS

<222> (1) .. (981)

<223> RDI01260

<400> 1

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gtc att tcc atg cca aca ccg ggc cag gtt ccg ttt tct gta gag ttt	96
Val Ile Ser Met Pro Thr Pro Gly Gln Val Pro Phe Ser Val Glu Phe	
20 25 30	
atg ccg cca cga gat gag gca gca gaa gag cga ctc tgg aaa gcc gcc	144
Met Pro Pro Arg Asp Glu Ala Ala Glu Glu Arg Leu Trp Lys Ala Ala	
35 40 45	
gaa gca ttt cac gac tta gga gcc tct ttt gtc tcc gtt act tat ggt	192
Glu Ala Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly	
50 55 60	
gca ggc gga tct agc cgc gag cgc aca atg cgt gtc gcg cac aag ctt	240
Ala Gly Gly Ser Ser Arg Glu Arg Thr Met Arg Val Ala His Lys Leu	
65 70 75 80	
tct cgt cat ccg ttg acc acg ctc gtt cat ctc acg ctt gtg gaa cac	288
Ser Arg His Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Glu His	
85 90 95	
acc caa gaa gaa tta gaa gaa att ctg tgc act tat gcg tcc cac ggg	336
Thr Gln Glu Glu Leu Glu Glu Ile Leu Cys Thr Tyr Ala Ser His Gly	
100 105 110	
ttg tct aac tta ctt gcc ttg cga ggc gat ccc cct ggc act gac ccg	384
Leu Ser Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Thr Asp Pro	
115 120 125	
atg gct ccg tgg gtc cct acc gca ggc ggc cta gat tat gcc aaa gat	432
Met Ala Pro Trp Val Pro Thr Ala Gly Gly Leu Asp Tyr Ala Lys Asp	
130 135 140	
ttg atc gac ctc gtg cgc aag act gag cag acc tcg cac ttt cag gta	480
Leu Ile Asp Leu Val Arg Lys Thr Glu Gln Thr Ser His Phe Gln Val	
145 150 155 160	

gga att gct agt ttc cca gaa ggg cac tac cga gcg cct agc att gag	528
Gly Ile Ala Ser Phe Pro Glu Gly His Tyr Arg Ala Pro Ser Ile Glu	
165 170 175	
gcg gat acg caa ttt aca ttg gaa aag ctg cga gct ggc gca gag ttt	576
Ala Asp Thr Gln Phe Thr Leu Glu Lys Leu Arg Ala Gly Ala Glu Phe	
180 185 190	
tcg att acc cag atg ttt ttt gat gtc gat cac tat tta cga ctg cga	624
Ser Ile Thr Gln Met Phe Phe Asp Val Asp His Tyr Leu Arg Leu Arg	
195 200 205	
gat cgc ttg gtt aag gcg gat cct gaa cat gga tca aag ccg atc atc	672
Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile	
210 215 220	
cca gga ctt atg ccc att acc agc ttg agg tcg gtt cgt agg cag atg	720
Pro Gly Leu Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Met	
225 230 235 240	
aa tta gca ggt gcc acc ttg cct aag gct tta gaa aaa cgg ctt ctc	768
lu Leu Ala Gly Ala Thr Leu Pro Lys Ala Leu Glu Lys Arg Leu Leu	
245 250 255	
gac gca gcg cgc ggc gat gag gaa gct cat cgc ggc gat att cgc aaa	816
Asp Ala Ala Arg Gly Asp Glu Glu Ala His Arg Gly Asp Ile Arg Lys	
260 265 270	
gta gga atc gaa gtc act act gag atg gca cag cgt ctt att tct gaa	864
Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu	
275 280 285	
ggg atc cca gac atc cat ttc atg acc atg aat tat gtt cga gcg acc	912
Gly Ile Pro Asp Ile His Phe Met Thr Met Asn Tyr Val Arg Ala Thr	
290 295 300	
caa gaa gta ctc cat aat ctc ggc atg gcg ccc gcg tgg gga aca cag	960
Gln Glu Val Leu His Asn Leu Gly Met Ala Pro Ala Trp Gly Thr Gln	
305 310 315 320	
aa ggc cac gac gct att cgc taa	984
ln Gly His Asp Ala Ile Arg	
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<210> 2
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 <213> corynebacterium diphteriae

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Val Ile Ser Met Pro Thr Pro Gly Gln Val Pro Phe Ser Val Glu Phe
20 25 30
Met Pro Pro Arg Asp Glu Ala Ala Glu Glu Arg Leu Trp Lys Ala Ala
35 40 45
Glu Ala Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
50 55 60

Ala Gly Gly Ser Ser Arg Glu Arg Thr Met Arg Val Ala His Lys Leu
 65 70 75 80
 Ser Arg His Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Glu His
 85 90 95
 Thr Gln Glu Glu Leu Glu Glu Ile Leu Cys Thr Tyr Ala Ser His Gly
 100 105 110
 Leu Ser Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Thr Asp Pro
 115 120 125
 Met Ala Pro Trp Val Pro Thr Ala Gly Gly Leu Asp Tyr Ala Lys Asp
 130 135 140
 Leu Ile Asp Leu Val Arg Lys Thr Glu Gln Thr Ser His Phe Gln Val
 145 150 155 160
 Gly Ile Ala Ser Phe Pro Glu Gly His Tyr Arg Ala Pro Ser Ile Glu
 165 170 175
 Ala Asp Thr Gln Phe Thr Leu Glu Lys Leu Arg Ala Gly Ala Glu Phe
 180 185 190
 Ser Ile Thr Gln Met Phe Phe Asp Val Asp His Tyr Leu Arg Leu Arg
 195 200 205
 Asp Arg Leu Val Lys Ala Asp Pro Glu His Gly Ser Lys Pro Ile Ile
 210 215 220
 Pro Gly Leu Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Met
 225 230 235 240
 Glu Leu Ala Gly Ala Thr Leu Pro Lys Ala Leu Glu Lys Arg Leu Leu
 245 250 255
 Asp Ala Ala Arg Gly Asp Glu Glu Ala His Arg Gly Asp Ile Arg Lys
 260 265 270
 Val Gly Ile Glu Val Thr Thr Glu Met Ala Gln Arg Leu Ile Ser Glu
 275 280 285
 Gly Ile Pro Asp Ile His Phe Met Thr Met Asn Tyr Val Arg Ala Thr
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 Gln Glu Val Leu His Asn Leu Gly Met Ala Pro Ala Trp Gly Thr Gln
 305 310 315 320
 Gln Gly His Asp Ala Ile Arg
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<210> 3
 <211> 924
 <212> DNA
 <213> Streptomyces lividans

<220>
 <221> CDS
 <222> (1) .. (921)
 <223> RSV00084

<400> 3

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cg t gac atc ctc gcc acc ggc aag acg acg tac tcg ttc gag ttc tcg	96
Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser	
20 25 30	
gcg ccg aag acg ccc aag ggc gag aag aac ctc tgg agc gcg ctg cgg	144
Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg	
35 40 45	
cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc	192
Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala	
50 55 60	
ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc	240
Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val	
65 70 75 80	
gc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac	288
Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His	
85 90 95	
tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg	336
Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly	
100 105 110	
atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac	384
Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn	
115 120 125	
gcc gac tgg atc gcg cac ccc gag ggc ctg acc tac gcg gcc gaa ctg	432
Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu	
130 135 140	
gtc agg ctc atc aag gag tcg gga gac ttc tgc gtc ggc gtc gcc gcc	480
Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala	
145 150 155 160	
tc ccc gag atg cac ccg cgc tcc gcc gac tgg gac acg gac gtc acg	528
he Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr	
165 170 175	
aac ttc gtc gac aag tgc cgg gcc ggc gcc gac tac gcc atc acc cag	576
Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln	
180 185 190	
atg ttc ttc cag ccc gac tcc tac ctc cgg ctg cgc gac cgg gtc gcc	624
Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala	
195 200 205	
gcg gcc ggc tgc gcg acc ccg gtc att ccc gag gtc atg ccg gtg acc	672
Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr	
210 215 220	
agt gtg aag atg ctg gag agg ttg ccg aag ctc agc aac gcc tcg ttc	720
Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe	
225 230 235 240	
ccg gcg gag ctg aaa gag cgg atc ctc aca gcc aag gac gat ccg gcg	768
Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala	

	245	250	255	
gct gta cgc tcg atc ggc atc gag ttc gcc acg gag ttc tgc gcg cgg				816
Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg				
	260	265	270	
ctg ctg gcc gag gga gtg cca gga ctg cac ttc atc acg ctc aac aac				864
Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn				
	275	280	285	
tcc acg gcg acg ctg gaa atc tac gag aac ctg ggc ctg cac cac cca				912
Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro				
	290	295	300	
ccg cgg gcc tag				924
Pro Arg Ala				
305				

<210> 4

<211> 307

<212> PRT

<213> Streptomyces lividans

<400> 4

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Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser				
20	25	30		
Ala Pro Lys Thr Pro Lys Gly Glu Lys Asn Leu Trp Ser Ala Leu Arg				
35	40	45		
Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala				
50	55	60		
Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val				
65	70	75	80	
Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His				
85	90	95		
Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly				
100	105	110		
Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn				
115	120	125		
Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu				
130	135	140		
Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala				
145	150	155	160	
Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr				
165	170	175		
Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln				
180	185	190		
Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala				
195	200	205		

Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
 210 215 220

Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
 225 230 235 240

Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
 245 250 255

Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
 260 265 270

Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
 275 280 285

Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
 290 295 300

Pro Arg Ala
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<210> 5
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 <212> DNA
 <213> Streptomyces coelicolor

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 <223> RSX01699

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cgt gac atc ctc gcc acc ggc aag acg acg tac tcg ttc gag ttc tcg 96
 Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser
 20 25 30

cgc ccg aag acg ccc aag ggc gag agg aac ctc tgg agc gcg ctg cgg 144
 Ala Pro Lys Thr Pro Lys Gly Glu Arg Asn Leu Trp Ser Ala Leu Arg
 35 40 45

cgg gtc gag gcc gtg gcc ccg gac ttc gtc tcc gtg acc tac ggc gcc 192
 Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
 50 55 60

ggc ggc tcc acg cgc gcc ggc acg gtc cgc gag acc cag cag atc gtc 240
 Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
 65 70 75 80

gcc gac acc acg ctg acc ccg gtg gcc cac ctc acc gcc gtc gac cac 288
 Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
 85 90 95

tcc gtc gcc gag ctg cgc aac atc atc ggc cag tac gcc gac gcc ggg 336
 Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
 100 105 110

atc cgc aac atg ctg gcc gtg cgc ggc gac ccg ccc ggc gac ccg aac 384

Ile	Arg	Asn	Met	Leu	Ala	Val	Arg	Gly	Asp	Pro	Pro	Gly	Asp	Pro	Asn	
		115					120					125				
gcc	gac	tgg	atc	gcg	cac	ccc	gag	ggc	ctg	acc	tac	gcg	gcc	gaa	ctg	432
Ala	Asp	Trp	Ile	Ala	His	Pro	Glu	Gly	Leu	Thr	Tyr	Ala	Ala	Glu	Leu	
	130					135					140					
gtc	agg	ctc	atc	aag	gag	tcg	ggc	gac	ttc	tgc	gtc	ggc	gtc	gcg	gcc	480
Val	Arg	Leu	Ile	Lys	Glu	Ser	Gly	Asp	Phe	Cys	Val	Gly	Val	Ala	Ala	
	145				150					155					160	
ttc	ccc	gag	atg	cac	ccg	cgc	tcc	gcc	gac	tgg	gac	acg	gac	gtc	acg	528
Phe	Pro	Glu	Met	His	Pro	Arg	Ser	Ala	Asp	Trp	Asp	Thr	Asp	Val	Thr	
				165					170					175		
aac	ttc	gtc	gac	aag	tgc	cgg	gcc	ggc	gcc	gac	tac	gcc	atc	acc	cag	576
Asn	Phe	Val	Asp	Lys	Cys	Arg	Ala	Gly	Ala	Asp	Tyr	Ala	Ile	Thr	Gln	
			180					185					190			
atg	ttc	ttc	cag	ccc	gac	tcc	tat	ctc	cgg	ctg	cgc	gac	cgg	gtc	gcc	624
Met	Phe	Phe	Gln	Pro	Asp	Ser	Tyr	Leu	Arg	Leu	Arg	Asp	Arg	Val	Ala	
		195					200					205				
gcg	gcc	ggc	tgc	gcg	acc	ccg	gtc	atc	ccc	gag	gtc	atg	ccg	gtg	acc	672
Ala	Ala	Gly	Cys	Ala	Thr	Pro	Val	Ile	Pro	Glu	Val	Met	Pro	Val	Thr	
	210					215					220					
agt	gtg	aag	atg	ctg	gag	agg	ttg	ccg	aag	ctc	agc	aac	gcc	tcg	ttc	720
Ser	Val	Lys	Met	Leu	Glu	Arg	Leu	Pro	Lys	Leu	Ser	Asn	Ala	Ser	Phe	
225					230				235						240	
ccg	gcg	gag	ttg	aaa	gag	cgg	atc	ctc	aca	gcc	aag	gac	gat	ccg	gcg	768
Pro	Ala	Glu	Leu	Lys	Glu	Arg	Ile	Leu	Thr	Ala	Lys	Asp	Asp	Pro	Ala	
				245					250					255		
gct	gta	cgc	tcg	atc	ggc	atc	gag	ttc	gcc	acg	gag	ttc	tgc	gcg	cgg	816
Ala	Val	Arg	Ser	Ile	Gly	Ile	Glu	Phe	Ala	Thr	Glu	Phe	Cys	Ala	Arg	
			260					265					270			
ctg	ctg	gcc	gag	gga	gtg	cca	gga	ctg	cac	ttc	atc	acg	ctc	aac	aac	864
Leu	Leu	Ala	Glu	Gly	Val	Pro	Gly	Leu	His	Phe	Ile	Thr	Leu	Asn	Asn	
		275					280					285				
tcc	acg	gcg	acg	ctg	gaa	atc	tac	gag	aac	ctg	ggc	ctg	cac	cac	cca	912
Ser	Thr	Ala	Thr	Leu	Glu	Ile	Tyr	Glu	Asn	Leu	Gly	Leu	His	His	Pro	
	290					295					300					
ccg	cgg	gcc	tag													924
Pro	Arg	Ala														
305																

<210> 6

<211> 307

<212> PRT

<213> Streptomyces coelicolor

<400> 6

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Arg Asp Ile Leu Ala Thr Gly Lys Thr Thr Tyr Ser Phe Glu Phe Ser

20

25

30

Ala Pro Lys Thr Pro Lys Gly Glu Arg Asn Leu Trp Ser Ala Leu Arg
35 40 45

Arg Val Glu Ala Val Ala Pro Asp Phe Val Ser Val Thr Tyr Gly Ala
50 55 60

Gly Gly Ser Thr Arg Ala Gly Thr Val Arg Glu Thr Gln Gln Ile Val
65 70 75 80

Ala Asp Thr Thr Leu Thr Pro Val Ala His Leu Thr Ala Val Asp His
85 90 95

Ser Val Ala Glu Leu Arg Asn Ile Ile Gly Gln Tyr Ala Asp Ala Gly
100 105 110

Ile Arg Asn Met Leu Ala Val Arg Gly Asp Pro Pro Gly Asp Pro Asn
115 120 125

Ala Asp Trp Ile Ala His Pro Glu Gly Leu Thr Tyr Ala Ala Glu Leu
130 135 140

Val Arg Leu Ile Lys Glu Ser Gly Asp Phe Cys Val Gly Val Ala Ala
145 150 155 160

Phe Pro Glu Met His Pro Arg Ser Ala Asp Trp Asp Thr Asp Val Thr
165 170 175

Asn Phe Val Asp Lys Cys Arg Ala Gly Ala Asp Tyr Ala Ile Thr Gln
180 185 190

Met Phe Phe Gln Pro Asp Ser Tyr Leu Arg Leu Arg Asp Arg Val Ala
195 200 205

Ala Ala Gly Cys Ala Thr Pro Val Ile Pro Glu Val Met Pro Val Thr
210 215 220

Ser Val Lys Met Leu Glu Arg Leu Pro Lys Leu Ser Asn Ala Ser Phe
225 230 235 240

Pro Ala Glu Leu Lys Glu Arg Ile Leu Thr Ala Lys Asp Asp Pro Ala
245 250 255

Ala Val Arg Ser Ile Gly Ile Glu Phe Ala Thr Glu Phe Cys Ala Arg
260 265 270

Leu Leu Ala Glu Gly Val Pro Gly Leu His Phe Ile Thr Leu Asn Asn
275 280 285

Ser Thr Ala Thr Leu Glu Ile Tyr Glu Asn Leu Gly Leu His His Pro
290 295 300

Pro Arg Ala
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<210> 7

<211> 891

<212> DNA

<213> Aquifex aeolicus

<220>

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 <222> (1) .. (888)
 <223> RAA00346

<400> 7

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 gag ttc ttt cca ccg aag act gaa gag gga gaa aga cag ctc ttt gaa	96
Glu Phe Phe Pro Pro Lys Thr Glu Glu Gly Glu Arg Gln Leu Phe Glu	
20 25 30	
 act ata agg aaa ctt gag aaa tta aat cct act ttt gta tcc gtt act	144
Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr	
35 40 45	
 tac ggg gca ggt ggt tcg act aga gat aga act agg aat ata gta cag	192
Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln	
50 55 60	
 a ata cac gag gaa act aac ctc acc gtt atg gca cac ctc acc tgt	240
ys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys	
65 70 75 80	
 ata gca cac acg aga gag gag ctt att gat atc ctt caa gat tac aaa	288
Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys	
85 90 95	
 aac ata ggt ata gag aac att ctc gct ttg agg ggg gac gtt ccg agg	336
Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg	
100 105 110	
 gac aaa ccg gac tgg aga ccg ccg aag ggt gcg tgc aag tat gca aaa	384
Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys	
115 120 125	
 gag ctc gta gaa ctg atc agg aag gag ttc gga gac tgg ttt tct atc	432
Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile	
130 135 140	
 a gtg gct tct tat cct gaa gga cat ccg gaa tca ccg aac ctc gag	480
y Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu	
145 150 155 160	
 tgg gaa gtg aag tac ttt aag gaa aag gta gag gca ggt gca gac ttc	528
Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe	
165 170 175	
 tcg att act cag atg ttt ttc gtg aac gat tac tac tac agg ttt gtg	576
Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val	
180 185 190	
 gaa atg tgc aaa aat gca ggg ata gat ata tct ata att ccg gga att	624
Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile	
195 200 205	
 atg cct att act aac ttc aaa cag ata aga aag ttt gct tct ctt tgc	672
Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys	
210 215 220	
 gga gcg acg att cca cag agt ctt ata gaa aag ctt gaa aaa gtg gag	720
Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu	

225	230	235	240	
gat aaa ccg gaa gaa gta aaa aag ata ggg att gag ttt gcc ata aat				768
Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn				
	245	250	255	
cag tgt ttg gat ctc ata gaa cac gga gtt ccg ggg ctt cac ttc tac				816
Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr				
	260	265	270	
act ctg aac aag tcc gac gca act ttg aag ata tac gag gct ata aag				864
Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys				
	275	280	285	
gat aaa ata ccg gcc cgt tca act taa				891
Asp Lys Ile Pro Ala Arg Ser Thr				
	290	295		

<210> 8
 <211> 296
 <212> PRT
 <213> Aquifex aeolicus

<400> 8

Met Lys Ile Gly Asp Ile Leu Arg Lys Gly Val Phe Ser Ile Ser Phe				
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Glu Phe Phe Pro Pro Lys Thr Glu Glu Gly Glu Arg Gln Leu Phe Glu				
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Thr Ile Arg Lys Leu Glu Lys Leu Asn Pro Thr Phe Val Ser Val Thr				
	35	40	45	
Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Arg Asn Ile Val Gln				
	50	55	60	
Lys Ile His Glu Glu Thr Asn Leu Thr Val Met Ala His Leu Thr Cys				
	65	70	75	80
Ile Ala His Thr Arg Glu Glu Leu Ile Asp Ile Leu Gln Asp Tyr Lys				
	85	90	95	
Asn Ile Gly Ile Glu Asn Ile Leu Ala Leu Arg Gly Asp Val Pro Arg				
	100	105	110	
Asp Lys Pro Asp Trp Arg Pro Pro Lys Gly Ala Cys Lys Tyr Ala Lys				
	115	120	125	
Glu Leu Val Glu Leu Ile Arg Lys Glu Phe Gly Asp Trp Phe Ser Ile				
	130	135	140	
Gly Val Ala Ser Tyr Pro Glu Gly His Pro Glu Ser Pro Asn Leu Glu				
	145	150	155	160
Trp Glu Val Lys Tyr Phe Lys Glu Lys Val Glu Ala Gly Ala Asp Phe				
	165	170	175	
Ser Ile Thr Gln Met Phe Phe Val Asn Asp Tyr Tyr Tyr Arg Phe Val				
	180	185	190	
Glu Met Cys Lys Asn Ala Gly Ile Asp Ile Ser Ile Ile Pro Gly Ile				
	195	200	205	

Met Pro Ile Thr Asn Phe Lys Gln Ile Arg Lys Phe Ala Ser Leu Cys
 210 215 220

Gly Ala Thr Ile Pro Gln Ser Leu Ile Glu Lys Leu Glu Lys Val Glu
 225 230 235 240

Asp Lys Pro Glu Glu Val Lys Lys Ile Gly Ile Glu Phe Ala Ile Asn
 245 250 255

Gln Cys Leu Asp Leu Ile Glu His Gly Val Pro Gly Leu His Phe Tyr
 260 265 270

Thr Leu Asn Lys Ser Asp Ala Thr Leu Lys Ile Tyr Glu Ala Ile Lys
 275 280 285

Asp Lys Ile Pro Ala Arg Ser Thr
 290 295

<210> 9
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 <212> DNA
 <213> Burkholderia cepacia

<220>
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 <223> RBU14992

<400> 9
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Met Asn Pro Ile Glu Leu Ser Phe Glu Phe Phe Pro Pro Lys Thr Gln
 1 5 10 15

gaa ggc gtg gac aag ctg cgc gcc acg cgc gcc cag ctc gcc acg ctc 96
 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
 20 25 30

aag ccc aag ttc gtg tcc gtc acg ttc ggc gcc ggc ggc tcg acg caa 144
 Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln
 35 40 45

cag ggc acg ctc gac acc gtc gtc gat atg gcg aag gaa ggg ctc gaa 192
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60

gcg gcg ccg cac gtg tcg tgc atc ggc tcg tcg aaa gag agc ctg cgc 240
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg
 65 70 75 80

gcc att ctc aac gag tac cgc gca cat ggc atc cgc cat atc gtc gcg 288

Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala
 85 90 95

ctg cgc ggc gat ctg ccg tcc ggc atg ggc gaa gtc ggc gag ctg cgc 336
 Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg
 100 105 110

tat gcg tcg gaa ctg gtg agc ttt atc cgc gcc gaa ttc ggc gac tgg 384
 Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp

115	120	125	
ttc tgc atc gag gtg gcc ggc tat ccg gaa tac cac ccg cag tcg cgc			432
Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg			
130	135	140	
tcg ccg cgt cag gat ctg gaa aac ttc gcc cgc aag gtg aag gcc ggc			480
Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly			
145	150	155	160
gcc aat tcg gcg atc aca cag tac ttc ttc aat gca gac gcg tat ttc			528
Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe			
165	170	175	
cgt ttc gtc gac gac gcg aga aag ctc gcc gtg gac gtg ccg atc gtg			576
Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val			
180	185	190	
ccg ggc atc atg ccg atc acg aac ttc tcg cag ctg atg cgt ttc tcg			624
Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser			
195	200	205	
ag atg tgc ggc gct gaa gtg cca cgc tgg atc gcg cgc cgg ctg gaa			672
Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu			
210	215	220	
agc ttc ggc gac gat cgc gag tca att cgc gcg ttc ggg ctg gat gtg			720
Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val			
225	230	235	240
gtg acg gac ctg tgc agg cgt ctg atc gat gcg aag gtg ccg ggc ctg			768
Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu			
245	250	255	
cac ttc tac acg cta aac ggc gca gcg gcg acc aag gcg atc tgc gaa			816
His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu			
260	265	270	
cgg ttg aac gtt taa			831
Arg Leu Asn Val			
275			

<210> 10
 <211> 276
 <212> PRT
 <213> Burkholderia cepacia

<400> 10
 Met Asn Pro Ile Glu Leu Ser Phe Glu Phe Phe Pro Pro Lys Thr Gln
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 Glu Gly Val Asp Lys Leu Arg Ala Thr Arg Ala Gln Leu Ala Thr Leu
 20 25 30
 Lys Pro Lys Phe Val Ser Val Thr Phe Gly Ala Gly Gly Ser Thr Gln
 35 40 45
 Gln Gly Thr Leu Asp Thr Val Val Asp Met Ala Lys Glu Gly Leu Glu
 50 55 60
 Ala Ala Pro His Val Ser Cys Ile Gly Ser Ser Lys Glu Ser Leu Arg

65	70	75	80
Ala Ile Leu Asn Glu Tyr Arg Ala His Gly Ile Arg His Ile Val Ala	85	90	95
Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Glu Val Gly Glu Leu Arg	100	105	110
Tyr Ala Ser Glu Leu Val Ser Phe Ile Arg Ala Glu Phe Gly Asp Trp	115	120	125
Phe Cys Ile Glu Val Ala Gly Tyr Pro Glu Tyr His Pro Gln Ser Arg	130	135	140
Ser Pro Arg Gln Asp Leu Glu Asn Phe Ala Arg Lys Val Lys Ala Gly	145	150	155
Ala Asn Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe	165	170	175
Arg Phe Val Asp Asp Ala Arg Lys Leu Gly Val Asp Val Pro Ile Val	180	185	190
Pro Gly Ile Met Pro Ile Thr Asn Phe Ser Gln Leu Met Arg Phe Ser	195	200	205
Glu Met Cys Gly Ala Glu Val Pro Arg Trp Ile Ala Arg Arg Leu Glu	210	215	220
Ser Phe Gly Asp Asp Arg Glu Ser Ile Arg Ala Phe Gly Leu Asp Val	225	230	235
Val Thr Asp Leu Cys Arg Arg Leu Ile Asp Ala Lys Val Pro Gly Leu	245	250	255
His Phe Tyr Thr Leu Asn Gly Ala Ala Ala Thr Lys Ala Ile Cys Glu	260	265	270
Arg Leu Asn Val	275		

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 <211> 846
 <212> DNA
 <213> Nitrosomonas europaea

<220>
 <221> CDS
 <222> (1)..(843)
 <223> RNE02657

<400> 11

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1 5 10 15	
ccg ccg cag aca ccg gaa ggc atg gaa aag ctg cgg gca acg cgc ata	96
Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile	
20 25 30	
cag ctt gct cag ttc aat ccg aag ttt ttt tcg gtg acg ttt ggt gcc	144

Gln	Leu	Ala	Gln	Phe	Asn	Pro	Lys	Phe	Phe	Ser	Val	Thr	Phe	Gly	Ala		
35						40						45					
ggc	gga	tcc	act	cgt	gaa	cgc	acg	ctc	gaa	acc	gtg	ctg	gaa	att	cag	192	
Gly	Gly	Ser	Thr	Arg	Glu	Arg	Thr	Leu	Glu	Thr	Val	Leu	Glu	Ile	Gln		
50						55			60								
gca	gaa	ggc	tat	ccg	gta	gcg	ccc	cat	ctt	tcc	tgt	atc	ggc	tcc	acg	240	
Ala	Glu	Gly	Tyr	Pro	Val	Ala	Pro	His	Leu	Ser	Cys	Ile	Gly	Ser	Thr		
65			70			75			80								
cgt	gac	aat	atc	cgt	tcg	atc	ctt	gag	aaa	tat	cac	agt	cac	ggc	atc	288	
Arg	Asp	Asn	Ile	Arg	Ser	Ile	Leu	Glu	Lys	Tyr	His	Ser	His	Gly	Ile		
			85			90			95								
agc	cgc	att	gtg	gcg	cta	cgt	ggc	gat	tta	ccc	tcc	ggc	atg	gcg	cag	336	
Ser	Arg	Ile	Val	Ala	Leu	Arg	Gly	Asp	Leu	Pro	Ser	Gly	Met	Ala	Gln		
			100			105			110								
gcg	gga	gaa	ttc	cgc	tac	gcc	aac	gag	ctg	gta	gca	ttt	atc	cgc	aag	384	
Ala	Gly	Glu	Phe	Arg	Tyr	Ala	Asn	Glu	Leu	Val	Ala	Phe	Ile	Arg	Lys		
115						120			125								
gag	ttc	ggc	gat	acc	ttc	tgg	atc	gaa	gtg	gcg	gct	tat	ccg	gaa	tat	432	
Glu	Phe	Gly	Asp	Thr	Phe	Trp	Ile	Glu	Val	Ala	Ala	Tyr	Pro	Glu	Tyr		
130						135			140								
cat	cca	caa	gcc	cgc	tcc	gct	ctg	gag	gat	ttc	acc	aat	ttc	aga	cga	480	
His	Pro	Gln	Ala	Arg	Ser	Ala	Leu	Glu	Asp	Phe	Thr	Asn	Phe	Arg	Arg		
145			150			155			160								
aaa	gtc	gaa	gca	ggc	tcc	aat	gca	gcg	att	acc	cag	ttt	ttc	tat	aac	528	
Lys	Val	Glu	Ala	Gly	Ser	Asn	Ala	Ala	Ile	Thr	Gln	Phe	Phe	Tyr	Asn		
			165			170			175								
gtg	gat	gcc	tat	ctg	cat	ttc	gta	gag	atg	tgt	gaa	gct	gcg	gat	ctg	576	
Val	Asp	Ala	Tyr	Leu	His	Phe	Val	Glu	Met	Cys	Glu	Ala	Ala	Asp	Leu		
			180			185			190								
aat	atc	ccg	atc	ggt	ccc	ggc	atc	atg	ccg	atc	agc	aaa	ttt	tct	caa	624	
Asn	Ile	Pro	Ile	Val	Pro	Gly	Ile	Met	Pro	Ile	Ser	Lys	Phe	Ser	Gln		
195						200			205								
ctg	gca	aga	ttt	tcg	gat	ggc	tgt	gga	gca	gaa	att	cca	cgc	tgg	att	672	
Leu	Ala	Arg	Phe	Ser	Asp	Gly	Cys	Gly	Ala	Glu	Ile	Pro	Arg	Trp	Ile		
210						215			220								
cgc	aga	aaa	ctg	gaa	agc	ttc	ggc	gat	gat	att	ccg	tct	atc	cag	gca	720	
Arg	Arg	Lys	Leu	Glu	Ser	Phe	Gly	Asp	Asp	Ile	Pro	Ser	Ile	Gln	Ala		
225			230			235			240								
ttc	ggg	ctg	gat	gtc	gtc	aca	gcg	tta	tgt	gct	cgt	ctg	ctg	gaa	gcc	768	
Phe	Gly	Leu	Asp	Val	Val	Thr	Ala	Leu	Cys	Ala	Arg	Leu	Leu	Glu	Ala		
			245			250			255								
ggc	gca	ccc	ggc	ctg	cat	ttc	tac	aca	ctc	aac	tcc	gcc	gta	cta	ccc	816	
Gly	Ala	Pro	Gly	Leu													

<210> 12
<211> 281
<212> PRT
<213> Nitrosomonas europaea

<400> 12

Met Gln Ser Gln Lys Lys Phe Thr Pro Thr Phe Ser Phe Glu Phe Phe
1 5 10 15

Pro Pro Gln Thr Pro Glu Gly Met Glu Lys Leu Arg Ala Thr Arg Ile
20 25 30

Gln Leu Ala Gln Phe Asn Pro Lys Phe Phe Ser Val Thr Phe Gly Ala
35 40 45

Gly Gly Ser Thr Arg Glu Arg Thr Leu Glu Thr Val Leu Glu Ile Gln
50 55 60

Ala Glu Gly Tyr Pro Val Ala Pro His Leu Ser Cys Ile Gly Ser Thr
65 70 75 80

Arg Asp Asn Ile Arg Ser Ile Leu Glu Lys Tyr His Ser His Gly Ile
85 90 95

Ser Arg Ile Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Ala Gln
100 105 110

Ala Gly Glu Phe Arg Tyr Ala Asn Glu Leu Val Ala Phe Ile Arg Lys
115 120 125

Glu Phe Gly Asp Thr Phe Trp Ile Glu Val Ala Ala Tyr Pro Glu Tyr
130 135 140

His Pro Gln Ala Arg Ser Ala Leu Glu Asp Phe Thr Asn Phe Arg Arg
145 150 155 160

Lys Val Glu Ala Gly Ser Asn Ala Ala Ile Thr Gln Phe Phe Tyr Asn
165 170 175

Ala Asp Ala Tyr Leu His Phe Val Glu Met Cys Glu Ala Ala Asp Leu
180 185 190

Asn Ile Pro Ile Val Pro Gly Ile Met Pro Ile Ser Lys Phe Ser Gln
195 200 205

Leu Ala Arg Phe Ser Asp Gly Cys Gly Ala Glu Ile Pro Arg Trp Ile
210 215 220

Arg Arg Lys Leu Glu Ser Phe Gly Asp Asp Ile Pro Ser Ile Gln Ala
225 230 235 240

Phe Gly Leu Asp Val Val Thr Ala Leu Cys Ala Arg Leu Leu Glu Ala
245 250 255

Gly Ala Pro Gly Leu His Phe Tyr Thr Leu Asn Ser Ala Val Leu Pro
260 265 270

Thr Lys Ile Trp Gln Arg Leu Gly Leu
275 280

<210> 13
 <211> 873
 <212> DNA
 <213> *Pseudomonas aeruginosa*

<220>
 <221> CDS
 <222> (1)..(870)
 <223> RPA03308

<400> 13
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 Val Val Ala Ser Lys Glu Pro Ile Met Ser Gln Ser Glu Arg Arg Phe
 1 5 10 15

agc ttc gag ttc ttc ccg gcg aag acc gag gcc ggc cat gaa aag ctg 96
 Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu
 20 25 30

ttg gcc acc gcc cgc aac ctg gcg ggc tac aag ccc gac ttc ttc tcc 144
 Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser
 35 40 45

tgc acc tac ggc gcc ggc gga tcc acc cgc gac cgc acg ttg agt acc 192
 Cys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr
 50 55 60

gtg ctg caa ctg gac ggc gag gtg aag gtg ccg acc gcg ccg cac ctg 240
 Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu
 65 70 75 80

tcc tgt gtc ggc gac tcg aaa gcc gag ttg cgc gaa ctg ctc ggc cgc 288
 Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg
 85 90 95

tac cgc gag gcc ggc atc cgc cgc atc gtc gcc ctg cgc ggc gac ctg 336
 Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu
 100 105 110

ccg tcg ggc atg ggc atg gcc agc ggc gaa ctg cgc tac gcc aac gaa 384
 Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu
 115 120 125

ctg gtg gac ttc atc cgc acc gag acc ggc gac cac ttc cac atc gag 432
 Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu
 130 135 140

gtc gcc gcc tat ccg gag gtc cac ccc cag gcg cgc agc ttc gag gat 480
 Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp
 145 150 155 160

gac ctg gcg aac ttc gtg cgc aag gtg aag gcc ggc gcc agc agc gcc 528
 Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala
 165 170 175

atc acc cag tac ttc ttc aac gcc gat gcc tat ttc tac ttc gtc gag 576
 Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu
 180 185 190

cgg gtc gcc aag ctc ggc gtg gac atc ccg gtg gtc ccc ggc atc atg 624
 Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met
 195 200 205

ccg atc acc aac tac tcc aag ctg gcg cgc ttc tcc gac gcc tgc ggc 672
 Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

gcc gaa ctg ccg cgc tgg atc cgc aag caa ctg gaa gcc tac ggc gac 720
 Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
 225 230 235 240

gac agc cgc agc atc cag gcc ttc ggc gag cag gtc atc agc gag atg 768
 Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

tgc gaa cgc ctg ctg gag ggc ggc gca ccg gga ctg cat ttc tat act 816
 Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
 260 265 270

ttg aac cag gcc gat ccg agc ctg gcg atc tgg aag aat ctc cag ctg 864
 Leu Asn Gln Ala Asp Pro Ser Leu Ala Ile Trp Lys Asn Leu Gln Leu
 275 280 285

ca cgc tga 873
 ro Arg
 290

<210> 14
 <211> 290
 <212> PRT
 <213> Pseudomonas aeruginosa

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Ser Phe Glu Phe Phe Pro Ala Lys Thr Glu Ala Gly His Glu Lys Leu
 20 25 30

Leu Ala Thr Ala Arg Asn Leu Ala Gly Tyr Lys Pro Asp Phe Phe Ser
 35 40 45

ys Thr Tyr Gly Ala Gly Gly Ser Thr Arg Asp Arg Thr Leu Ser Thr
 50 55 60

Val Leu Gln Leu Asp Gly Glu Val Lys Val Pro Thr Ala Pro His Leu
 65 70 75 80

Ser Cys Val Gly Asp Ser Lys Ala Glu Leu Arg Glu Leu Leu Gly Arg
 85 90 95

Tyr Arg Glu Ala Gly Ile Arg Arg Ile Val Ala Leu Arg Gly Asp Leu
 100 105 110

Pro Ser Gly Met Gly Met Ala Ser Gly Glu Leu Arg Tyr Ala Asn Glu
 115 120 125

Leu Val Asp Phe Ile Arg Thr Glu Thr Gly Asp His Phe His Ile Glu
 130 135 140

Val Ala Ala Tyr Pro Glu Val His Pro Gln Ala Arg Ser Phe Glu Asp
 145 150 155 160

Asp Leu Ala Asn Phe Val Arg Lys Val Lys Ala Gly Ala Ser Ser Ala

165

170

175

Ile Thr Gln Tyr Phe Phe Asn Ala Asp Ala Tyr Phe Tyr Phe Val Glu
 180 185 190

Arg Val Ala Lys Leu Gly Val Asp Ile Pro Val Val Pro Gly Ile Met
 195 200 205

Pro Ile Thr Asn Tyr Ser Lys Leu Ala Arg Phe Ser Asp Ala Cys Gly
 210 215 220

Ala Glu Leu Pro Arg Trp Ile Arg Lys Gln Leu Glu Ala Tyr Gly Asp
 225 230 235 240

Asp Ser Arg Ser Ile Gln Ala Phe Gly Glu Gln Val Ile Ser Glu Met
 245 250 255

Cys Glu Arg Leu Leu Glu Gly Gly Ala Pro Gly Leu His Phe Tyr Thr
 260 265 270

Leu Asn Gln Ala Asp Pro Ser Leu Ala Ile Trp Lys Asn Leu Gln Leu
 275 280 285

Pro Arg
 290

<210> 15
 <211> 828
 <212> DNA
 <213> Xylella almond

<220>
 <221> CDS
 <222> (1)..(825)
 <223> RXFX00359

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 1 5 10 15

cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca 96
 Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro
 20 25 30

gaa tac gtc tcc tgc acc ttc ggc gcc ggt ggc tcc aca ctc agt tac 144
 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

acc tca gaa aca gtg cgc cat ctc agc caa cac cac ggc ttt gac gcc 192
 Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala
 50 55 60

gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa 240
 Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
 65 70 75 80

ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta 288
 Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
 85 90 95

cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt acc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tat aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
he Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	
caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct	672
Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
210 215 220	
tac ggc gac gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg	720
Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
225 230 235 240	
acc gca tta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac	768
Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	
ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc	816
he Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg	
260 265 270	
tta ggc tat tga	828
Leu Gly Tyr	
275	

<210> 16
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 <212> PRT
 <213> Xylella almond

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 Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr
 35 40 45

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Ala

50

55

60

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu
65 70 75 80

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu
85 90 95

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr
100 105 110

Ala Ala Asp Leu Ile Thr Phe Ile Arg Thr Glu His Gly Asp His Phe
115 120 125

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn
130 135 140

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala
145 150 155 160

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His
165 170 175

Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala
180 185 190

Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu
195 200 205

Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala
210 215 220

Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val
225 230 235 240

Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His
245 250 255

Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
260 265 270

Leu Gly Tyr
275

<210> 17
<211> 828
<212> DNA
<213> Xylella oleander

<220>
<221> CDS
<222> (1)..(825)
<223> RXFY01676

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1 5 10 15

cgc gca cag ttg gac agg aca gca aac cgg cta cgc gca ttc gca cca	96
Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro	
20 25 30	
gaa tac gtc tcc tgc acc ttc ggc gcc ggc ggc tcc aca ctc agt tac	144
Glu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr	
35 40 45	
acc tca gaa aca gtg cgc cat ctc agt caa cac cac ggc ttt gac acc	192
Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr	
50 55 60	
gca ccg cat ctg tcc tgt gtg ggc ggc agt cgc caa gaa atc cgc gaa	240
Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu	
65 70 75 80	
ctt ctc aaa ctg tac cgc gcg att ggc tgc caa cgc atc gtg gcg cta	288
Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
85 90 95	
cgc ggc gat ctc ccc tcg ggc atg ggc cac ccc ggc gac ctc cgc tac	336
Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	
gca gct gac ctg att acc ttc atc cgt gcc gag cat ggc gat cac ttc	384
Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe	
115 120 125	
cac cta gag atc ggc gca tac ccg gaa acc cac cca caa gcc agc aac	432
His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	
aca ctg aac gac ctt cac tat ttc aaa gcc aaa gcc gat gca ggc gcc	480
Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	
gat gcg gca atc act caa tac ttt tac aac cca gac gcc tat ttc cac	528
Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	
ttc gtc gac gca gtg cag cgc ctg ggc gtc acc atc ccc att gtt gcc	576
Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	
gga gtc atg ccc atc tcc aac ttt gac cag ttg cgc cat ttc tcc gaa	624
Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	
caa tgc ggc gcc gaa ata ccc cgc tgg att aca aaa aaa atg cag gct	672
Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
210 215 220	
tac ggc gat gac acc aaa tcg ata cgc gcg ttc ggt gcc gac gtc gtg	720
Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
225 230 235 240	
acc gca cta tgt gag cgg cta atc gct ggc ggc gca ccg ggg ctg cac	768
Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	

ttc tac acg ctc aac cta gcc aaa cca agc acc caa gtg ctg caa cgc	816
Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg	
260 265 270	

tta ggc tat tga	828
Leu Gly Tyr	
275	

<210> 18
 <211> 275
 <212> PRT
 <213> Xylella oleander

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Arg Ala Gln Leu Asp Arg Thr Ala Asn Arg Leu Arg Ala Phe Ala Pro	
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Leu Tyr Val Ser Cys Thr Phe Gly Ala Gly Gly Ser Thr Leu Ser Tyr	
35 40 45	

Thr Ser Glu Thr Val Arg His Leu Ser Gln His His Gly Phe Asp Thr	
50 55 60	

Ala Pro His Leu Ser Cys Val Gly Gly Ser Arg Gln Glu Ile Arg Glu	
65 70 75 80	

Leu Leu Lys Leu Tyr Arg Ala Ile Gly Cys Gln Arg Ile Val Ala Leu	
85 90 95	

Arg Gly Asp Leu Pro Ser Gly Met Gly His Pro Gly Asp Leu Arg Tyr	
100 105 110	

Ala Ala Asp Leu Ile Thr Phe Ile Arg Ala Glu His Gly Asp His Phe	
115 120 125	

His Leu Glu Ile Gly Ala Tyr Pro Glu Thr His Pro Gln Ala Ser Asn	
130 135 140	

Thr Leu Asn Asp Leu His Tyr Phe Lys Ala Lys Ala Asp Ala Gly Ala	
145 150 155 160	

Asp Ala Ala Ile Thr Gln Tyr Phe Tyr Asn Pro Asp Ala Tyr Phe His	
165 170 175	

Phe Val Asp Ala Val Gln Arg Leu Gly Val Thr Ile Pro Ile Val Ala	
180 185 190	

Gly Val Met Pro Ile Ser Asn Phe Asp Gln Leu Arg His Phe Ser Glu	
195 200 205	

Gln Cys Gly Ala Glu Ile Pro Arg Trp Ile Thr Lys Lys Met Gln Ala	
210 215 220	

Tyr Gly Asp Asp Thr Lys Ser Ile Arg Ala Phe Gly Ala Asp Val Val	
225 230 235 240	

Thr Ala Leu Cys Glu Arg Leu Ile Ala Gly Gly Ala Pro Gly Leu His	
245 250 255	

Phe Tyr Thr Leu Asn Leu Ala Lys Pro Ser Thr Gln Val Leu Gln Arg
 260 265 270

Leu Gly Tyr
 275

<210> 19
 <211> 846

<212> DNA
 <213> *Pseudomonas fluorescens*

<220>
 <221> CDS
 <222> (1)..(843)
 <223> RPU04845

<400> 19

ctg tcc caa gac cgt cgc tac agc ttc gag ttc ttc ccg acc aag acc	48
t Ser Gln Asp Arg Arg Tyr Ser Phe Glu Phe Phe Pro Thr Lys Thr	
1 5 10 15	
gat gct ggg cat gaa aaa ctg ctc gcc act gcc cgt cag ctg gcc acc	96
Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr	
20 25 30	
tat aag cct gac ttc ttt tcc tgc acc tac ggc gct ggc ggt tcg acc	144
Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr	
35 40 45	
cgt gac cgc acg ctg aac acc gtt ctg cag ctg gaa agc gaa gtc aaa	192
Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys	
50 55 60	
atc ccc gcc gca ccg cac ctg tcg tgc gtc ggc gac agc aag gac gac	240
Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp	
65 70 75 80	
ctg cgc ggc ctg ctg aac gag tac aag gcc gcc ggc atc aag cgc atc	288
Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile	
85 90 95	
gtc gcc ctg cgc ggt gac ctg ccg tcc ggc atg ggc atg acc agc ggc	336
Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly	
100 105 110	
gag ctg cgt cac gcc aat gaa ctg gtt gaa ttc att cgt gaa gaa acc	384
Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr	
115 120 125	
ggc aat cat ttc cac atc gaa gtc gcc gcc tac ccg gag atg cat ccg	432
Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro	
130 135 140	
caa gcg cgc aac tac gaa gac gat ctc gcc aac ttc gtg cgc aag gcc	480
Gln Ala Arg Asn Tyr Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala	
145 150 155 160	
cgt gcc ggc gcc gac agc gcg atc acc cag tac ttc ttc aac gcc gac	528
Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp	
165 170 175	

agc tac ttc tac ttc gtc gac cgt ttg cag gcg ctg ggc gtg gac att 576
 Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile
 180 185 190

ccg gtg gta ccg ggg atc atg ccg atc acc aac tac agc aaa ctc gcg 624
 Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala
 195 200 205

cgc ttc tcc gat gcc tgc ggt gcg gaa atc ccg cgc tgg atc cgc aag 672
 Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys
 210 215 220

cag ctg gaa gcc tac ggc gat gac agc caa agc att cag cgc ttt ggc 720
 Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly
 225 230 235 240

gaa caa gtc gtc acg gaa atg tgc gaa cgc ctg ctg caa ggc ggc gcg 768
 Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala
 245 250 255

cgc ggc ctg cac ttc tat tcc atg aac cag gcc gaa cca agc ctg gcg 816
 Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala
 260 265 270

atc tgg aac aac ctg aag ctg ccg cgc taa 846
 Ile Trp Asn Asn Leu Lys Leu Pro Arg
 275 280

<210> 20
 <211> 281
 <212> PRT
 <213> *Pseudomonas fluorescens*

<400> 20
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Asp Ala Gly His Glu Lys Leu Leu Ala Thr Ala Arg Gln Leu Ala Thr
 20 25 30

Tyr Lys Pro Asp Phe Phe Ser Cys Thr Tyr Gly Ala Gly Gly Ser Thr
 35 40 45

Arg Asp Arg Thr Leu Asn Thr Val Leu Gln Leu Glu Ser Glu Val Lys
 50 55 60

Ile Pro Ala Ala Pro His Leu Ser Cys Val Gly Asp Ser Lys Asp Asp
 65 70 75 80

Leu Arg Gly Leu Leu Asn Glu Tyr Lys Ala Ala Gly Ile Lys Arg Ile
 85 90 95

Val Ala Leu Arg Gly Asp Leu Pro Ser Gly Met Gly Met Thr Ser Gly
 100 105 110

Glu Leu Arg His Ala Asn Glu Leu Val Glu Phe Ile Arg Glu Glu Thr
 115 120 125

Gly Asn His Phe His Ile Glu Val Ala Ala Tyr Pro Glu Met His Pro
 130 135 140

Gln Ala Arg Asn Tyr	Glu Asp Asp Leu Ala Asn Phe Val Arg Lys Ala	
145	150	155 160
Arg Ala Gly Ala Asp Ser Ala Ile Thr Gln Tyr Phe Phe Asn Ala Asp		
165	170	175
Ser Tyr Phe Tyr Phe Val Asp Arg Leu Gln Ala Leu Gly Val Asp Ile		
180	185	190
Pro Val Val Pro Gly Ile Met Pro Ile Thr Asn Tyr Ser Lys Leu Ala		
195	200	205
Arg Phe Ser Asp Ala Cys Gly Ala Glu Ile Pro Arg Trp Ile Arg Lys		
210	215	220
Gln Leu Glu Ala Tyr Gly Asp Asp Ser Gln Ser Ile Gln Arg Phe Gly		
225	230	235 240
Glu Gln Val Val Thr Glu Met Cys Glu Arg Leu Leu Gln Gly Gly Ala		
245	250	255
Pro Gly Leu His Phe Tyr Ser Met Asn Gln Ala Glu Pro Ser Leu Ala		
260	265	270
Ile Trp Asn Asn Leu Lys Leu Pro Arg		
275	280	

<210> 21
 <211> 1812
 <212> DNA
 <213> Schizosaccharomyces pombe

<220>
 <221> CDS
 <222> (1) .. (1809)
 <223> RSO01645

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1 5 10 15	
act tac agt tat gaa ttt ttt cct cca aaa acg agc act ggt gtc caa	96
Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln	
20 25 30	
aat ctt tac aat cgt ata gat cgc atg aag act tgg ggt cgt ccc atg	144
Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met	
35 40 45	
ttt gtc gat gtg act tgg ggt gct ggt ggt act tct tca gaa ctg act	192
Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr	
50 55 60	
cct gga atc gtt aat gta att caa aca gat ttt gaa gtg gat act tgc	240
Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys	
65 70 75 80	
atg cat ttg act tgt acg aac atg tcc aca gaa atg att gac gca gct	288
Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala	
85 90 95	

ttg aaa cgg gct cat gaa aca ggg tgt cgt aac ata ttg gcc ctt aga	336
Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg	
100 105 110	
ggt gat cct gtt aaa gat aca gac tgg act gaa ggc gaa agt gga ttc	384
Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe	
115 120 125	
cgg tat gct tca gac tta gtt aga tat att cgc aca cat tat aat gat	432
Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp	
130 135 140	
gaa ttc tgt att ggt gta gct ggc tat cca gaa gga tat tca cca gat	480
Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp	
145 150 155 160	
gat gac att gat gaa agc ata aag cat ctg aaa tta aaa gtc gat gaa	528
Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu	
165 170 175	
ggt gct gat ttt atc gtt act caa atg ttt tat gat gta gac aat ttt	576
Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe	
180 185 190	
atc gca tgg gtc gat aaa gtg cgt gca gca gga ata aat atc cct ata	624
Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile	
195 200 205	
ttt ccg ggc att atg cct att cag gca tgg gat tcc ttt att ccg aga	672
Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg	
210 215 220	
gcg aaa tgg agc ggt gtt aaa att ccc cag cat ttt atg gat act cta	720
Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu	
225 230 235 240	
gtc cca gtt aaa gac gat gat gaa gga gtc cgt gag cgt ggt gtt gag	768
Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu	
245 250 255	
ctc ata gtc gaa atg tgc cgt aag ctt ata gct agt ggc att acg aga	816
Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg	
260 265 270	
ctt cat ttt tac act atg aat tta gaa aag gcc gtt aaa atg att att	864
Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile	
275 280 285	
gaa cga tta ggt tta tta gat gaa aac ttg gct cct ata gtg gat act	912
Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr	
290 295 300	
aat aac gtc gag tta acc aat gct tcc agt caa gat cgt cgg ata aat	960
Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn	
305 310 315 320	
gaa ggt gta cgg ccc att ttc tgg cgc act cgt aat gaa agt tat gtc	1008
Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val	
325 330 335	
tcg cgt act gat cag tgg gac gaa tta ccg cat ggt cgt tgg ggt gac	1056
Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp	
340 345 350	

tct cgt agc cct gct ttt ggc gaa ttt gat gct att aga tat ggt ctt Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu 355 360 365	1104
cgt atg tct ccc aag gag atc aca aca tcg tgg ggg tct cct aaa tct Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser 370 375 380	1152
tac tcg gaa atc ggc gat ttg ttt gcc agg tac tgt gaa aaa aag att Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile 385 390 395 400	1200
agc tcc ctc cct tgg agt gat ctt ccc ata tcc gat gaa gcc gac ttg Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu 405 410 415	1248
att cgg gat caa ctt cta agt atg aat aga aac gct ttc ctt act ata Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile 420 425 430	1296
t tct caa cct gct ctt aac ggc gaa aag agt tca cat cct gtt ttt en Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe 435 440 445	1344
gga tgg gga cca cct aat ggt tat gtt ttc caa aaa cca tac gtt gag Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu 450 455 460	1392
ttt ttc gtt cac ccc tca ctc ttg aat gaa ctc aaa gaa acc gtt aaa Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys 465 470 475 480	1440
aag ctt aat tca gtt tcc tac ttt gtt aca aac aag aat gga gac ttg Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu 485 490 495	1488
gat acc aac tca caa tat gag att cca aat gcg gtt aca tgg ggt gtt Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val 500 505 510	1536
tc cct aat cgt gag att atc caa cct act att gtc gag tca acc tct ne Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser 515 520 525	1584
ttt ctt gct tgg aaa gat gaa gcc tat tca ttg ggc atg gaa tgg gct Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala 530 535 540	1632
aat gca tat agc cct gat tca att tct cgt aaa ctt ttg gtt tct atg Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met 545 550 555 560	1680
atg aag gaa tgg ttc ctt tgt gtc ata gtt gat aac gat ttt caa aat Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn 565 570 575	1728
ggg caa tct ttg ttt gat gtt ttt aac aaa atg aga tct tta aaa gac Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp 580 585 590	1776
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<210> 22
 <211> 603
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 22

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Thr Tyr Ser Tyr Glu Phe Phe Pro Pro Lys Thr Ser Thr Gly Val Gln
 20 25 30

Asn Leu Tyr Asn Arg Ile Asp Arg Met Lys Thr Trp Gly Arg Pro Met
 35 40 45

Phe Val Asp Val Thr Trp Gly Ala Gly Gly Thr Ser Ser Glu Leu Thr
 50 55 60

Pro Gly Ile Val Asn Val Ile Gln Thr Asp Phe Glu Val Asp Thr Cys
 65 70 75 80

Met His Leu Thr Cys Thr Asn Met Ser Thr Glu Met Ile Asp Ala Ala
 85 90 95

Leu Lys Arg Ala His Glu Thr Gly Cys Arg Asn Ile Leu Ala Leu Arg
 100 105 110

Gly Asp Pro Val Lys Asp Thr Asp Trp Thr Glu Gly Glu Ser Gly Phe
 115 120 125

Arg Tyr Ala Ser Asp Leu Val Arg Tyr Ile Arg Thr His Tyr Asn Asp
 130 135 140

Glu Phe Cys Ile Gly Val Ala Gly Tyr Pro Glu Gly Tyr Ser Pro Asp
 145 150 155 160

Asp Asp Ile Asp Glu Ser Ile Lys His Leu Lys Leu Lys Val Asp Glu
 165 170 175

Gly Ala Asp Phe Ile Val Thr Gln Met Phe Tyr Asp Val Asp Asn Phe
 180 185 190

Ile Ala Trp Val Asp Lys Val Arg Ala Ala Gly Ile Asn Ile Pro Ile
 195 200 205

Phe Pro Gly Ile Met Pro Ile Gln Ala Trp Asp Ser Phe Ile Arg Arg
 210 215 220

Ala Lys Trp Ser Gly Val Lys Ile Pro Gln His Phe Met Asp Thr Leu
 225 230 235 240

Val Pro Val Lys Asp Asp Asp Glu Gly Val Arg Glu Arg Gly Val Glu
 245 250 255

Leu Ile Val Glu Met Cys Arg Lys Leu Ile Ala Ser Gly Ile Thr Arg
 260 265 270

Leu His Phe Tyr Thr Met Asn Leu Glu Lys Ala Val Lys Met Ile Ile
 275 280 285

Glu Arg Leu Gly Leu Leu Asp Glu Asn Leu Ala Pro Ile Val Asp Thr
 290 295 300
 Asn Asn Val Glu Leu Thr Asn Ala Ser Ser Gln Asp Arg Arg Ile Asn
 305 310 315 320
 Glu Gly Val Arg Pro Ile Phe Trp Arg Thr Arg Asn Glu Ser Tyr Val
 325 330 335
 Ser Arg Thr Asp Gln Trp Asp Glu Leu Pro His Gly Arg Trp Gly Asp
 340 345 350
 Ser Arg Ser Pro Ala Phe Gly Glu Phe Asp Ala Ile Arg Tyr Gly Leu
 355 360 365
 Arg Met Ser Pro Lys Glu Ile Thr Thr Ser Trp Gly Ser Pro Lys Ser
 370 375 380
 Tyr Ser Glu Ile Gly Asp Leu Phe Ala Arg Tyr Cys Glu Lys Lys Ile
 385 390 395 400
 Ser Ser Leu Pro Trp Ser Asp Leu Pro Ile Ser Asp Glu Ala Asp Leu
 405 410 415
 Ile Arg Asp Gln Leu Leu Ser Met Asn Arg Asn Ala Phe Leu Thr Ile
 420 425 430
 Asn Ser Gln Pro Ala Leu Asn Gly Glu Lys Ser Ser His Pro Val Phe
 435 440 445
 Gly Trp Gly Pro Pro Asn Gly Tyr Val Phe Gln Lys Pro Tyr Val Glu
 450 455 460
 Phe Phe Val His Pro Ser Leu Leu Asn Glu Leu Lys Glu Thr Val Lys
 465 470 475 480
 Lys Leu Asn Ser Val Ser Tyr Phe Val Thr Asn Lys Asn Gly Asp Leu
 485 490 495
 Asp Thr Asn Ser Gln Tyr Glu Ile Pro Asn Ala Val Thr Trp Gly Val
 500 505 510
 Ser Pro Asn Arg Glu Ile Ile Gln Pro Thr Ile Val Glu Ser Thr Ser
 515 520 525
 Phe Leu Ala Trp Lys Asp Glu Ala Tyr Ser Leu Gly Met Glu Trp Ala
 530 535 540
 Asn Ala Tyr Ser Pro Asp Ser Ile Ser Arg Lys Leu Leu Val Ser Met
 545 550 555 560
 Met Lys Glu Trp Phe Leu Cys Val Ile Val Asp Asn Asp Phe Gln Asn
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 Gly Gln Ser Leu Phe Asp Val Phe Asn Lys Met Arg Ser Leu Lys Asp
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 Ile His Pro Glu Leu Tyr Tyr Ala Asn Ala Ser
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<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1797)
<223> RSC08323

<400> 23

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ccc act tac tca ttc gag tac ttc gtc ccg aag act aca caa ggt gta	96
Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val	
20 25 30	
cag aac ctg tat gac cgg atg gac cgg atg tac gag gct tct ttg ccc	144
Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro	
35 40 45	
aaa ttt att gac atc acc tgg aat gca ggc ggt gga cgg ttg tca cat	192
Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His	
50 55 60	
ctg tcc acg gac ttg gtt gcg aca gcg cag tct gtg ctt ggt ttg gaa	240
Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu	
65 70 75 80	
acg tgc atg cac ctt acc tgc acc aat atg ccc att tcg atg att gac	288
Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp	
85 90 95	
gac gct tta gaa aac gct tat cac tcc ggt tgc cag aac atc cta gcg	336
Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala	
100 105 110	
ctg aga gga gat cct cct agg gac gca gaa aac tgg act ccc gtt gaa	384
Leu Arg Gly Asp Pro Pro Arg Asp Ala Glu Asn Trp Thr Pro Val Glu	
115 120 125	
gtg ggc ttc cag tat gcc aag gac ttg att aag tat atc aag tcc aag	432
Gly Gly Phe Gln Tyr Ala Lys Asp Leu Ile Lys Tyr Ile Lys Ser Lys	
130 135 140	
tac ggt gac cat ttc gct atc ggc gtt gcc ggc tac ccg gag tgc cat	480
Tyr Gly Asp His Phe Ala Ile Gly Val Ala Gly Tyr Pro Glu Cys His	
145 150 155 160	
ccg gag ttg cct aac aaa gac gtg aag ctt gat ctc gag tat ttg agc	528
Pro Glu Leu Pro Asn Lys Asp Val Lys Leu Asp Leu Glu Tyr Leu Ser	
165 170 175	
aga aga tcg acc ggc ggc gac ttc atc atc act cag atg ttt tac gat	576
Arg Arg Ser Thr Gly Gly Asp Phe Ile Ile Thr Gln Met Phe Tyr Asp	
180 185 190	
gtt gat aat tta ctc aac tgg tgt tcc caa gtt aga gct gcg ggc atg	624
Val Asp Asn Leu Leu Asn Trp Cys Ser Gln Val Arg Ala Ala Gly Met	
195 200 205	
gac gtg ccc att att ccc ggg atc atg ccg atc act acc tac gcg gcc	672

Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala		
210						215					220						
ttc	ttg	aga	agg	atc	caa	tgg	ggc	caa	atc	tcc	atc	cct	caa	cat	ttc	720	
Phe	Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe		
225					230					235					240		
tcg	tcc	cga	ttg	gat	cct	atc	aag	gac	gat	gac	gag	ttg	gtc	cgt	gat	768	
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp		
				245					250					255			
atc	gga	act	aac	ttg	atc	gtg	gaa	atg	tgt	caa	aaa	ttg	ctc	gac	agt	816	
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser		
			260					265					270				
ggc	tac	gtt	tct	cac	ttg	cac	atc	tac	acc	atg	aac	ttg	gaa	aaa	gcg	864	
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala		
		275					280					285					
cct	ctc	atg	att	ctg	gaa	aga	ttg	aac	att	cta	cct	acg	gaa	tca	gag	912	
Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu		
		290				295					300						
ttc	aat	gca	cat	cca	ttg	gcc	gtg	ttg	cca	tgg	aga	aaa	tct	ttg	aat	960	
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn		
305					310					315					320		
cca	aag	cgt	aaa	aac	gag	gaa	gtc	aga	cct	atc	ttc	tgg	aag	aga	aga	1008	
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg		
				325					330					335			
cct	tac	tcc	tat	gtc	gca	aga	acc	tct	caa	tgg	gcc	gtg	gac	gaa	ttc	1056	
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe		
			340					345					350				
ccc	aac	ggc	aga	ttc	ggc	gat	tcg	tct	tct	cct	gcg	ttc	ggc	gac	ttg	1104	
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu		
		355				360						365					
gat	ctg	tgt	ggc	tca	gac	ttg	atc	agg	caa	tca	gcg	aac	aaa	tgt	ctc	1152	
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu		
		370				375					380						
gaa	tta	tgg	tcc	acc	cct	act	tcc	atc	aac	gac	gtc	gcc	ttc	ttg	gtc	1200	
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val		
385					390					395					400		
atc	aac	tac	ttg	aat	gga	aac	ttg	aag	tgt	tta	cct	tgg	agt	gat	atc	1248	
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile		
				405				410						415			
ccc	atc	aat	gat	gaa	ata	aat	cca	atc	aaa	gca	cac	ttg	att	gag	ctg	1296	
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu		
			420					425					430				
aac	cag	cat	tct	atc	atc	act	ata	aac	tct	caa	cct	caa	gtc	aac	ggc	1344	
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly		
		435					440					445					
att	agg	tcc	aat	gac	aaa	att	cat	ggc	tgg	gga	ccc	aag	gat	ggc	tac	1392	
Ile	Arg	Ser	Asn	Asp	Lys	Ile	His	Gly	Trp	Gly	Pro	Lys	Asp	Gly	Tyr		
		450				455					460						

gtt tac cag aag caa tat ttg gaa ttt atg ttg ccc aag act aag ttg	1440
Val Tyr Gln Lys Gln Tyr Leu Glu Phe Met Leu Pro Lys Thr Lys Leu	
465 470 475 480	
ccc aag ttg att gac acc ttg aaa aac aat gag ttc ttg acc tac ttc	1488
Pro Lys Leu Ile Asp Thr Leu Lys Asn Asn Glu Phe Leu Thr Tyr Phe	
485 490 495	
gcc atc gac tct caa ggt gac ctg cta agt aat cat cca gac aac tcc	1536
Ala Ile Asp Ser Gln Gly Asp Leu Ser Asn His Pro Asp Asn Ser	
500 505 510	
aag tcc aac gct gtg act tgg ggt att ttc ccc ggc aga gaa att ctt	1584
Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu	
515 520 525	
caa cct acc att gtc gag aaa att tcg ttc tta gcg tgg aag gag gag	1632
Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu	
530 535 540	
ttc tat cat atc ttg aat gaa tgg aaa cta aac atg aat aaa tac gat	1680
Ile Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp	
545 550 555 560	
aaa ccg cat agt gcc caa ttc att cag tcc ttg att gac gat tac tgc	1728
Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys	
565 570 575	
ttg gtc aat att gtt gac aat gac tac att tct cca gat gat caa atc	1776
Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile	
580 585 590	
cat tcc atc cta cta agc cta taa	1800
His Ser Ile Leu Leu Ser Leu	
595	

<210> 24

<211> 599

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 24

Met Lys Ile Thr Glu Lys Leu Glu Gln His Arg Gln Thr Ser Gly Lys	
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Pro Thr Tyr Ser Phe Glu Tyr Phe Val Pro Lys Thr Thr Gln Gly Val	
20 25 30	
Gln Asn Leu Tyr Asp Arg Met Asp Arg Met Tyr Glu Ala Ser Leu Pro	
35 40 45	
Gln Phe Ile Asp Ile Thr Trp Asn Ala Gly Gly Gly Arg Leu Ser His	
50 55 60	
Leu Ser Thr Asp Leu Val Ala Thr Ala Gln Ser Val Leu Gly Leu Glu	
65 70 75 80	
Thr Cys Met His Leu Thr Cys Thr Asn Met Pro Ile Ser Met Ile Asp	
85 90 95	
Asp Ala Leu Glu Asn Ala Tyr His Ser Gly Cys Gln Asn Ile Leu Ala	
100 105 110	

Leu	Arg	Gly	Asp	Pro	Pro	Arg	Asp	Ala	Glu	Asn	Trp	Thr	Pro	Val	Glu		
		115					120					125					
Gly	Gly	Phe	Gln	Tyr	Ala	Lys	Asp	Leu	Ile	Lys	Tyr	Ile	Lys	Ser	Lys		
		130				135					140						
Tyr	Gly	Asp	His	Phe	Ala	Ile	Gly	Val	Ala	Gly	Tyr	Pro	Glu	Cys	His		
145					150					155					160		
Pro	Glu	Leu	Pro	Asn	Lys	Asp	Val	Lys	Leu	Asp	Leu	Glu	Tyr	Leu	Ser		
				165					170						175		
Arg	Arg	Ser	Thr	Gly	Gly	Asp	Phe	Ile	Ile	Thr	Gln	Met	Phe	Tyr	Asp		
			180					185						190			
Val	Asp	Asn	Leu	Leu	Asn	Trp	Cys	Ser	Gln	Val	Arg	Ala	Ala	Gly	Met		
		195					200					205					
Asp	Val	Pro	Ile	Ile	Pro	Gly	Ile	Met	Pro	Ile	Thr	Thr	Tyr	Ala	Ala		
		210				215					220						
Leu	Arg	Arg	Ile	Gln	Trp	Gly	Gln	Ile	Ser	Ile	Pro	Gln	His	Phe			
225				230					235					240			
Ser	Ser	Arg	Leu	Asp	Pro	Ile	Lys	Asp	Asp	Asp	Glu	Leu	Val	Arg	Asp		
				245					250					255			
Ile	Gly	Thr	Asn	Leu	Ile	Val	Glu	Met	Cys	Gln	Lys	Leu	Leu	Asp	Ser		
			260					265						270			
Gly	Tyr	Val	Ser	His	Leu	His	Ile	Tyr	Thr	Met	Asn	Leu	Glu	Lys	Ala		
		275					280					285					
Pro	Leu	Met	Ile	Leu	Glu	Arg	Leu	Asn	Ile	Leu	Pro	Thr	Glu	Ser	Glu		
		290				295					300						
Phe	Asn	Ala	His	Pro	Leu	Ala	Val	Leu	Pro	Trp	Arg	Lys	Ser	Leu	Asn		
305					310					315					320		
Pro	Lys	Arg	Lys	Asn	Glu	Glu	Val	Arg	Pro	Ile	Phe	Trp	Lys	Arg	Arg		
				325					330					335			
Pro	Tyr	Ser	Tyr	Val	Ala	Arg	Thr	Ser	Gln	Trp	Ala	Val	Asp	Glu	Phe		
			340					345					350				
Pro	Asn	Gly	Arg	Phe	Gly	Asp	Ser	Ser	Ser	Pro	Ala	Phe	Gly	Asp	Leu		
		355					360						365				
Asp	Leu	Cys	Gly	Ser	Asp	Leu	Ile	Arg	Gln	Ser	Ala	Asn	Lys	Cys	Leu		
		370				375					380						
Glu	Leu	Trp	Ser	Thr	Pro	Thr	Ser	Ile	Asn	Asp	Val	Ala	Phe	Leu	Val		
385					390					395					400		
Ile	Asn	Tyr	Leu	Asn	Gly	Asn	Leu	Lys	Cys	Leu	Pro	Trp	Ser	Asp	Ile		
				405					410					415			
Pro	Ile	Asn	Asp	Glu	Ile	Asn	Pro	Ile	Lys	Ala	His	Leu	Ile	Glu	Leu		
			420					425					430				
Asn	Gln	His	Ser	Ile	Ile	Thr	Ile	Asn	Ser	Gln	Pro	Gln	Val	Asn	Gly		
		435					440					445					

Ile Arg Ser Asn Asp Lys Ile His Gly Trp Gly Pro Lys Asp Gly Tyr
 450 455 460
 Val Tyr Gln Lys Gln Tyr Leu Glu Phe Met Leu Pro Lys Thr Lys Leu
 465 470 475 480
 Pro Lys Leu Ile Asp Thr Leu Lys Asn Asn Glu Phe Leu Thr Tyr Phe
 485 490 495
 Ala Ile Asp Ser Gln Gly Asp Leu Leu Ser Asn His Pro Asp Asn Ser
 500 505 510
 Lys Ser Asn Ala Val Thr Trp Gly Ile Phe Pro Gly Arg Glu Ile Leu
 515 520 525
 Gln Pro Thr Ile Val Glu Lys Ile Ser Phe Leu Ala Trp Lys Glu Glu
 530 535 540
 Phe Tyr His Ile Leu Asn Glu Trp Lys Leu Asn Met Asn Lys Tyr Asp
 545 550 555 560
 Lys Pro His Ser Ala Gln Phe Ile Gln Ser Leu Ile Asp Asp Tyr Cys
 565 570 575
 Leu Val Asn Ile Val Asp Asn Asp Tyr Ile Ser Pro Asp Asp Gln Ile
 580 585 590
 His Ser Ile Leu Leu Ser Leu
 595

<210> 25
 <211> 897
 <212> DNA
 <213> Erwinia carotovora

<220>
 <221> CDS
 <222> (1)..(894)
 <223> REO00089

400> 25
 atg agc ttt ttt cac gca aac cag cgg gaa gcg ctg aat caa agt ctg 48
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15
 gcg gaa ttg cag gga cga att aat gtg tca ttt gaa ttt ttc ccg cca 96
 Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 cgt acc agc gat atg gaa gaa acc ctg tgg agc tct atc gat cga ctg 144
 Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu
 35 40 45
 agc agc ctg aag ccc aag ttt gtt tcc gtg act tac ggg gcg aat tct 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 ggc gag cgt gac cgt act cac agc att atc aaa acg att aaa gag cgt 240
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg
 65 70 75 80

acc ggt ctg gaa gcg gca cct cac ctg acc tgc atc gat gct tca cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
gaa cag ctg cgt gaa atc gct cag gat tac tgg gag agt ggt atc cgc	336
Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg	
100 105 110	
cat att gtc gcg ctg cgc ggc gac ttg cct caa gaa ggc ggc aaa ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro	
115 120 125	
gac atg tac gcg gcg gat ctg gtt tcc ctg ctg aaa gag gtc ggt gat	432
Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp	
130 135 140	
ttc gat att tcc gtt gcc gcc tat cct gaa gta cac cct gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
ggc gcg cag gct gac ctg att aac ctg aaa cac aag att gat gcc ggc	528
Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly	
165 170 175	
gcg aat cgc gct atc aca cag ttc ttt ttc gac gta gaa agc tat ttg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgg ttc cgt gac cgc tgc gtg gca acg ggc atc gat gta gaa att gtg	624
Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val	
195 200 205	
ccg ggc att ctg cca gta tgc aac ttc aaa cag ttg cag aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala	
210 215 220	
acg atg acc aac gtc cgt gtg ccg aac tgg atg acg acc atg ttt gac	720
Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp	
225 230 235 240	
ggc ctg gat aac gat cca gaa acc cgc aaa atg gtg ggg gcg tct atc	768
Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile	
245 250 255	
gcc atg gat atg gtg aaa att ctc agc cgc gaa ggc gta aaa gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	
cat ttc tat acg ctg aac cgc gcg gag ctg agc tat gcg att tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His	
275 280 285	
acg ctg ggc gtc cgc cct gat gta gca cgc tga	897
Thr Leu Gly Val Arg Pro Asp Val Ala Arg	
290 295	

<210> 26

<211> 298

<212> PRT

<213> Erwinia carotovora

<400> 26

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15
 Ala Glu Leu Gln Gly Arg Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 Arg Thr Ser Asp Met Glu Glu Thr Leu Trp Ser Ser Ile Asp Arg Leu
 35 40 45
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Thr Ile Lys Glu Arg
 65 70 75 80
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
 85 90 95
 Glu Gln Leu Arg Glu Ile Ala Gln Asp Tyr Trp Glu Ser Gly Ile Arg
 100 105 110
 s Ile Val Ala Leu Arg Gly Asp Leu Pro Gln Glu Gly Gly Lys Pro
 115 120 125
 Asp Met Tyr Ala Ala Asp Leu Val Ser Leu Leu Lys Glu Val Gly Asp
 130 135 140
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160
 Ser Ala Gln Ala Asp Leu Ile Asn Leu Lys His Lys Ile Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ala Thr Gly Ile Asp Val Glu Ile Val
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Leu Gln Lys Phe Ala
 210 215 220
 Thr Met Thr Asn Val Arg Val Pro Asn Trp Met Thr Thr Met Phe Asp
 225 230 235 240
 Gly Leu Asp Asn Asp Pro Glu Thr Arg Lys Met Val Gly Ala Ser Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Leu Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Asp Val Ala Arg
 290 295

<210> 27

<211> 888

<212> DNA

<213> *Klebsiella pneumoniae*

<220>
 <221> CDS
 <222> (1)..(885)
 <223> RKP07488

<400> 27

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1 5 10 15	
gcg gaa gtc cag ggc cag att aat gtg tct ttt gaa ttc ttt ccg ccg	96
Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aaa tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tcg gta acc tat ggc gcg aac tct	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
gc gag cgc gat cgc acc cac agc atc atc aaa ggc att aaa gag cga	240
Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
acc ggt ctg gaa gca gcg ccg cac ctg acc tgt atc gat gcc agc cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg	
85 90 95	
gat gag ttg cgc act atc gct cag gat tac tgg aac aac ggt atc cgc	336
Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cat atc gtc gcc ctg cgc ggc gac ctg ccg ccg ggc agc ggt aaa ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gat atg tac gcc gcc gat ctg gtg acg ttg ctg aaa gag gta ggc gat	432
Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp	
130 135 140	
ct gat atc tct gtc gcc gcg tat ccg gaa gtg cat ccg gag gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcg gat tta ctg aac ctg aag cgc aaa gta gaa gca ggg	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly	
165 170 175	
gcc aac cgc gcg atc acc cag ttc ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gat cgc tgc gtc tcg gca ggc atc gac gtg gaa atc att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccc ggt atc ctg ccg gtc tcc aac ttt aaa cag gcg aaa aag ttt gcg	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aac gtc cgt atc ccg gtg tgg atg tca aaa atg ttc gaa	720

Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu	
225	230 235 240
ggg ctg gat aac gac gcc gaa acc cgt caa ctg gtg ggg gcg aat atc	768
Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile	
	245 250 255
gcc atg gac atg gtg aag atc tta agc cgg gaa ggg gtc aag gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
	260 265 270
cac ttc tac acc ctg aac cgc gcc gag atg agc tac gcc atc tgc cat	864
His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His	
	275 280 285
acg ctg ggc gta cgc ccg gcc tga	888
Thr Leu Gly Val Arg Pro Ala	
	290 295

<210> 28

<211> 295

<212> PRT

<213> Klebsiella pneumoniae

<400> 28

Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
1 5 10 15

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Lys Ser Ile Asp Arg Leu
35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
50 55 60

Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Glu Arg
65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Ser Arg
85 90 95

Asp Glu Leu Arg Thr Ile Ala Gln Asp Tyr Trp Asn Asn Gly Ile Arg
100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
115 120 125

Asp Met Tyr Ala Ala Asp Leu Val Thr Leu Leu Lys Glu Val Gly Asp
130 135 140

Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Glu Ala Gly
165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile

195

200

205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

Asp Met Thr Asn Val Arg Ile Pro Val Trp Met Ser Lys Met Phe Glu
 225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Gln Leu Val Gly Ala Asn Ile
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

Thr Leu Gly Val Arg Pro Ala
 290 295

<10> 29
 <211> 891
 <212> DNA
 <213> Salmonella typhi

<220>
 <221> CDS
 <222> (1)..(888)
 <223> RTY02485

<400> 29
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 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
 1 5 10 15

gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg 96
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg 144
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

agc agc ctg aaa ccg aag ttt gtt tcg gta acg tat ggc gcc aac tcc 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

ggg gaa cgt gac cgc act cat agt gtt att aaa ggc att aaa gag cgt 240
 Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc 288
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95

gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc 336
 Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

cac att gtt gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg 384
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gtc gat 432
 Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp
 130 135 140

ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa 480
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc 528
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175

gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tat ctg 576
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

cgt ttt cgc gac cgc tgt gtt tcc gcc ggt atc gac gta gaa att att 624
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205

c ggc att tta ccg gtg tct aac ttt aaa cag gcg aaa aaa ttt gcc 672
 o Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

gat atg acc aat gtc cgc att ccg tcc tgg atg tcg ctg atg ttt gag 720
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240

ggg ctg gat gat gac gca gaa acc cgc aag ctg gtg ggc gct aac att 768
 Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255

gcg atg gac atg gtg aaa att tta agc cgc gaa gga gtg aag gat ttc 816
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

cg ctg ggc gta aga ccg ggt tta taa 891
 hr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 30
 <211> 296
 <212> PRT
 <213> Salmonella typhi

<400> 30
 Met Ser Phe Phe His Ala Asn Gln Arg Glu Ala Leu Asn Gln Ser Leu
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Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95
 Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125
 Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Val Asp
 130 135 140
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240
 Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 31
 <211> 891
 <212> DNA
 <213> Salmonella typhimurium

<220>
 <221> CDS
 <222> (1)..(888)
 <223> RSY00593

<400> 31
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 1 5 10 15
 gcg gaa gta cag ggt cag att aac gtt tcg ttt gaa ttt ttc ccg ccg 96

Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro	
20 25 30	
cgc acc agt gaa atg gag caa acc ctg tgg aac tcc atc gat cgc ctg	144
Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu	
35 40 45	
agc agt ctg aaa ccg aag ttt gtt tgc gta acg tat ggc gcc aac tcc	192
Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser	
50 55 60	
ggg gaa cgc gac cgc acc cat agc gtt att aaa ggc atc aaa gag cgt	240
Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg	
65 70 75 80	
act ggg ctt gag gcc gcg ccg cac ctt acc tgt att gac gcc acg cgc	288
Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg	
85 90 95	
gat gaa ctg cgc acc atc gcc cgc gac tac tgg aat aac ggt atc cgc	336
asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg	
100 105 110	
cac att gtc gct ttg cgc ggc gat ttg ccg ccg ggc agc ggt aag ccg	384
His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro	
115 120 125	
gag atg tac gcc gcc gat ctg gtt ggt ttg ctc aaa gag gtg gcc gat	432
Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp	
130 135 140	
ttc gat att tca gta gcg gcc tat ccg gag gta cat ccg gaa gcg aaa	480
Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys	
145 150 155 160	
agc gcg cag gcc gat ctg ctt aat ctg aag cgt aaa gtg gat gct ggc	528
Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly	
165 170 175	
gct aac cgc gcg ata acc caa ttt ttc ttc gat gtg gaa agc tac ctg	576
Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu	
180 185 190	
cgt ttt cgc gac cgc tgt gtt tct gcc ggt atc gac gta gaa att att	624
Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile	
195 200 205	
ccc ggc att tta ccg gtg tct aac ttt aaa cag gca aaa aaa ttt gcc	672
Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala	
210 215 220	
gat atg acc aat gtc cgc att ccg tcc tgg atg tca ctg atg ttt gag	720
Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu	
225 230 235 240	
ggg ctg gat aat gac gca gaa acc cgc aag ctg gtg ggc gct aac att	768
Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile	
245 250 255	
gcg atg gac atg gtg aaa att tta agc cgt gaa gga gtg aag gat ttc	816
Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe	
260 265 270	

cac ttc tac acg ttg aat cgt gcg gaa atg agt tat gcc att tgc cac 864
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

acg ctg ggc gta aga ccg ggt tta taa 891
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 32
 <211> 296
 <212> PRT
 <213> Salmonella typhimurium

<400> 32
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Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

g Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

Gly Glu Arg Asp Arg Thr His Ser Val Ile Lys Gly Ile Lys Glu Arg
 65 70 75 80

Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Arg
 85 90 95

Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

Glu Met Tyr Ala Ala Asp Leu Val Gly Leu Leu Lys Glu Val Ala Asp
 130 135 140

he Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175

Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190

Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205

Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220

Asp Met Thr Asn Val Arg Ile Pro Ser Trp Met Ser Leu Met Phe Glu
 225 230 235 240

Gly Leu Asp Asn Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255

Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270

His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285

Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 33
 <211> 891
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1) .. (888)
 <223> REC03839

400> 33
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 et Ser Phe Phe His Ala Ser Gln Arg Asp Ala Leu Asn Gln Ser Leu
 1 5 10 15

gca gaa gtc cag ggg cag att aac gtt tcg ttc gag ttt ttc ccg ccg 96
 Ala Glu Val Gln Gly Gln Ile Asn Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30

cgt acc agt gaa atg gag cag acc ctg tgg aac tcc atc gat cgc ctt 144
 Arg Thr Ser Glu Met Glu Gln Thr Leu Trp Asn Ser Ile Asp Arg Leu
 35 40 45

agc agc ctg aaa ccg aag ttt gta tcg gtg acc tat ggc gcg aac tcc 192
 Ser Ser Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser
 50 55 60

ggc gag cgc gac cgt acg cac agc att att aaa ggc att aaa gat cgc 240
 Gly Glu Arg Asp Arg Thr His Ser Ile Ile Lys Gly Ile Lys Asp Arg
 65 70 75 80

ct ggt ctg gaa gcg gca ccg cat ctt act tgc att gat gcg acg ccc 288
 Thr Gly Leu Glu Ala Ala Pro His Leu Thr Cys Ile Asp Ala Thr Pro
 85 90 95

gac gag ctg cgc acc att gca cgc gac tac tgg aat aac ggt att cgt 336
 Asp Glu Leu Arg Thr Ile Ala Arg Asp Tyr Trp Asn Asn Gly Ile Arg
 100 105 110

cat atc gtg gcg ctg cgt ggc gat ctg ccg ccg gga agt ggt aag cca 384
 His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125

gaa atg tat gct tct gac ctg gtg acg ctg tta aaa gaa gtg gca gat 432
 Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp
 130 135 140

ttc gat atc tcc gtg gcg gcg tat ccg gaa gtt cac ccg gaa gca aaa 480
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160

agc gct cag gcg gat ttg ctt aat ctg aaa cgc aaa gtg gat gcc gga 528

Ser	Ala	Gln	Ala	Asp	Leu	Leu	Asn	Leu	Lys	Arg	Lys	Val	Asp	Ala	Gly	
				165					170					175		
gcc	aac	cgc	gcg	att	act	cag	ttc	ttc	ttc	gat	gtc	gaa	agc	tac	ctg	576
Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu	
			180					185					190			
cgt	ttt	cgt	gac	cgc	tgt	gta	tcg	gcg	ggc	att	gat	gtg	gaa	att	att	624
Arg	Phe	Arg	Asp	Arg	Cys	Val	Ser	Ala	Gly	Ile	Asp	Val	Glu	Ile	Ile	
		195					200					205				
ccg	gga	att	ttg	ccg	gta	tct	aac	ttt	aaa	cag	gcg	aag	aaa	ttt	gcc	672
Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn	Phe	Lys	Gln	Ala	Lys	Lys	Phe	Ala	
	210					215					220					
gat	atg	acc	aac	gtg	cgt	att	ccg	gcg	tgg	atg	gcg	caa	atg	ttc	gac	720
Asp	Met	Thr	Asn	Val	Arg	Ile	Pro	Ala	Trp	Met	Ala	Gln	Met	Phe	Asp	
225					230				235					240		
ggc	ctg	gat	gat	gat	gcc	gaa	acc	cgc	aaa	ctg	gtt	ggc	gcg	aat	att	768
Gly	Leu	Asp	Asp	Asp	Ala	Glu	Thr	Arg	Lys	Leu	Val	Gly	Ala	Asn	Ile	
				245					250					255		
gcc	atg	gat	atg	gtg	aag	att	tta	agc	cgt	gaa	gga	gtg	aaa	gat	ttc	816
Ala	Met	Asp	Met	Val	Lys	Ile	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	
			260					265					270			
cac	ttc	tat	acg	ctt	aac	cgt	gct	gaa	atg	agt	tac	gcg	att	tgc	cat	864
His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala	Glu	Met	Ser	Tyr	Ala	Ile	Cys	His	
		275				280						285				
acg	ctg	ggg	gtt	cga	cct	ggc	tta	taa								891
Thr	Leu	Gly	Val	Arg	Pro	Gly	Leu									
	290					295										

<210> 34
 <211> 296
 <212> PRT
 <213> Escherichia coli

400> 34																
Met	Ser	Phe	Phe	His	Ala	Ser	Gln	Arg	Asp	Ala	Leu	Asn	Gln	Ser	Leu	
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Ala	Glu	Val	Gln	Gly	Gln	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	
			20					25						30		
Arg	Thr	Ser	Glu	Met	Glu	Gln	Thr	Leu	Trp	Asn	Ser	Ile	Asp	Arg	Leu	
		35					40						45			
Ser	Ser	Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	
		50				55					60					
Gly	Glu	Arg	Asp	Arg	Thr	His	Ser	Ile	Ile	Lys	Gly	Ile	Lys	Asp	Arg	
65					70					75				80		
Thr	Gly	Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Cys	Ile	Asp	Ala	Thr	Pro	
				85					90					95		
Asp	Glu	Leu	Arg	Thr	Ile	Ala	Arg	Asp	Tyr	Trp	Asn	Asn	Gly	Ile	Arg	
		100						105					110			

His Ile Val Ala Leu Arg Gly Asp Leu Pro Pro Gly Ser Gly Lys Pro
 115 120 125
 Glu Met Tyr Ala Ser Asp Leu Val Thr Leu Leu Lys Glu Val Ala Asp
 130 135 140
 Phe Asp Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys
 145 150 155 160
 Ser Ala Gln Ala Asp Leu Leu Asn Leu Lys Arg Lys Val Asp Ala Gly
 165 170 175
 Ala Asn Arg Ala Ile Thr Gln Phe Phe Phe Asp Val Glu Ser Tyr Leu
 180 185 190
 Arg Phe Arg Asp Arg Cys Val Ser Ala Gly Ile Asp Val Glu Ile Ile
 195 200 205
 Pro Gly Ile Leu Pro Val Ser Asn Phe Lys Gln Ala Lys Lys Phe Ala
 210 215 220
 p Met Thr Asn Val Arg Ile Pro Ala Trp Met Ala Gln Met Phe Asp
 225 230 235 240
 Gly Leu Asp Asp Asp Ala Glu Thr Arg Lys Leu Val Gly Ala Asn Ile
 245 250 255
 Ala Met Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Lys Asp Phe
 260 265 270
 His Phe Tyr Thr Leu Asn Arg Ala Glu Met Ser Tyr Ala Ile Cys His
 275 280 285
 Thr Leu Gly Val Arg Pro Gly Leu
 290 295

<210> 35
 <211> 915
 <212> DNA
 <213> *Vibrio cholerae*

<220>
 <221> CDS
 <222> (1)..(912)
 <223> RVC06433

<400> 35
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 Val Thr Leu Gly His Arg Glu Tyr Lys Met Gly Tyr Thr His Ala Ser
 1 5 10 15
 cat atc gat gca ttg aac caa aac att gcg gag ctt tcc gac atc aat 96
 His Ile Asp Ala Leu Asn Gln Asn Ile Ala Glu Leu Ser Asp Ile Asn
 20 25 30
 gtt tcg ttt gag ttt ttt cca ccc agc tca cca caa atg gaa gaa acg 144
 Val Ser Phe Glu Phe Phe Pro Pro Ser Ser Pro Gln Met Glu Glu Thr
 35 40 45
 ctt tgg gga tcg gta cac cgt ctg aaa aca ctc caa ccg aaa ttt gtt 192
 Leu Trp Gly Ser Val His Arg Leu Lys Thr Leu Gln Pro Lys Phe Val
 50 55 60

tcg gtc act tat ggt gca aac tct ggt gag cgt gac cgt act cac tcg	240
Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu Arg Asp Arg Thr His Ser	
65 70 75 80	
atc att aaa gcg atc aaa gat caa acc ggt tta att gcc gcg cca cac	288
Ile Ile Lys Ala Ile Lys Asp Gln Thr Gly Leu Ile Ala Ala Pro His	
85 90 95	
ctg act tgt atc gat gcc act cgt gat gaa ctg atc cag atc gcc gat	336
Leu Thr Cys Ile Asp Ala Thr Arg Asp Glu Leu Ile Gln Ile Ala Asp	
100 105 110	
gac tac tgg cat aac ggc atc cag aat att gtg gcg ctg cgt ggg gat	384
Asp Tyr Trp His Asn Gly Ile Gln Asn Ile Val Ala Leu Arg Gly Asp	
115 120 125	
atc ccg gct ggc ggt ggt aag cca gag atg tac gcc tcc gat cta gtg	432
Ile Pro Ala Gly Gly Gly Lys Pro Glu Met Tyr Ala Ser Asp Leu Val	
130 135 140	
g ctg ctc aaa tca cgc cac gat ttt gat att tcc gtg gcc gcc ttc	480
Leu Leu Lys Ser Arg His Asp Phe Asp Ile Ser Val Ala Ala Phe	
145 150 155 160	
cct gaa gtg cac cct gaa gcc aaa agc gcg caa gcg gac ctg ctc aat	528
Pro Glu Val His Pro Glu Ala Lys Ser Ala Gln Ala Asp Leu Leu Asn	
165 170 175	
tta aaa cgt aaa gtc gat gca ggt gcg aat cgt gcc atc acg cag ttt	576
Leu Lys Arg Lys Val Asp Ala Gly Ala Asn Arg Ala Ile Thr Gln Phe	
180 185 190	
ttc ttt gat gta gaa agc tac ctg cgt ttt cgc gat cgc tgt gtg gcc	624
Phe Phe Asp Val Glu Ser Tyr Leu Arg Phe Arg Asp Arg Cys Val Ala	
195 200 205	
gct ggg att gac gta gaa atc gtg cct ggc att ctg ccg gtt tct aac	672
Ala Gly Ile Asp Val Glu Ile Val Pro Gly Ile Leu Pro Val Ser Asn	
210 215 220	
ctt aaa caa gcg tcg cgc ttc gct gcg caa aac aac gtc aaa gtt ccg	720
Leu Lys Gln Ala Ser Arg Phe Ala Ala Gln Asn Asn Val Lys Val Pro	
225 230 235 240	
aat tgg atg gtg aag cag ttt gaa gga tta gaa gac gat cca gtg act	768
Asn Trp Met Val Lys Gln Phe Glu Gly Leu Glu Asp Asp Pro Val Thr	
245 250 255	
cgc cag ttg gta ggt gca agc caa gcc att gat atg gtg cgc gtg ctg	816
Arg Gln Leu Val Gly Ala Ser Gln Ala Ile Asp Met Val Arg Val Leu	
260 265 270	
tgc cgt gaa ggg gtg aag gat ttc cac ttc tac acc cta aat cgt gcc	864
Cys Arg Glu Gly Val Lys Asp Phe His Phe Tyr Thr Leu Asn Arg Ala	
275 280 285	
gaa atg act tac gcg tta tgc cac acc tta ggc gtt cgc cca caa gct	912
Glu Met Thr Tyr Ala Leu Cys His Thr Leu Gly Val Arg Pro Gln Ala	
290 295 300	
taa	915

<210> 36
<211> 304
<212> PRT
<213> Vibrio cholerae

<400> 36

Val	Thr	Leu	Gly	His	Arg	Glu	Tyr	Lys	Met	Gly	Tyr	Thr	His	Ala	Ser
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His	Ile	Asp	Ala	Leu	Asn	Gln	Asn	Ile	Ala	Glu	Leu	Ser	Asp	Ile	Asn
			20					25					30		
Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Ser	Ser	Pro	Gln	Met	Glu	Glu	Thr
		35					40					45			
Leu	Trp	Gly	Ser	Val	His	Arg	Leu	Lys	Thr	Leu	Gln	Pro	Lys	Phe	Val
	50					55					60				
Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	Gly	Glu	Arg	Asp	Arg	Thr	His	Ser
65					70				75						80
Ile	Ile	Lys	Ala	Ile	Lys	Asp	Gln	Thr	Gly	Leu	Ile	Ala	Ala	Pro	His
				85					90					95	
Leu	Thr	Cys	Ile	Asp	Ala	Thr	Arg	Asp	Glu	Leu	Ile	Gln	Ile	Ala	Asp
		100						105					110		
Asp	Tyr	Trp	His	Asn	Gly	Ile	Gln	Asn	Ile	Val	Ala	Leu	Arg	Gly	Asp
		115					120					125			
Ile	Pro	Ala	Gly	Gly	Gly	Lys	Pro	Glu	Met	Tyr	Ala	Ser	Asp	Leu	Val
	130					135						140			
Thr	Leu	Leu	Lys	Ser	Arg	His	Asp	Phe	Asp	Ile	Ser	Val	Ala	Ala	Phe
145					150					155					160
Pro	Glu	Val	His	Pro	Glu	Ala	Lys	Ser	Ala	Gln	Ala	Asp	Leu	Leu	Asn
			165						170				175		
Leu	Lys	Arg	Lys	Val	Asp	Ala	Gly	Ala	Asn	Arg	Ala	Ile	Thr	Gln	Phe
			180					185					190		
Phe	Phe	Asp	Val	Glu	Ser	Tyr	Leu	Arg	Phe	Arg	Asp	Arg	Cys	Val	Ala
		195					200					205			
Ala	Gly	Ile	Asp	Val	Glu	Ile	Val	Pro	Gly	Ile	Leu	Pro	Val	Ser	Asn
	210					215					220				
Phe	Lys	Gln	Ala	Ser	Arg	Phe	Ala	Ala	Gln	Asn	Asn	Val	Lys	Val	Pro
225					230					235					240
Asn	Trp	Met	Val	Lys	Gln	Phe	Glu	Gly	Leu	Glu	Asp	Asp	Pro	Val	Thr
			245						250					255	
Arg	Gln	Leu	Val	Gly	Ala	Ser	Gln	Ala	Ile	Asp	Met	Val	Arg	Val	Leu
			260					265					270		
Cys	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe	Tyr	Thr	Leu	Asn	Arg	Ala
		275					280						285		
Glu	Met	Thr	Tyr	Ala	Leu	Cys	His	Thr	Leu	Gly	Val	Arg	Pro	Gln	Ala
	290					295						300			

<210> 37
 <211> 879
 <212> DNA
 <213> Haemophilus influenzae

<220>
 <221> CDS
 <222> (1)..(876)
 <223> RHI06620

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 1 5 10 15
 att aat aaa aaa att aat gtc tcc ttt gaa ttt ttt cca cct aaa aac 96
 e Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn
 20 25 30
 gaa aaa atg gaa acc ctt cta tgg gat tca att cat cgt tta aaa gta 144
 Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val
 35 40 45
 tta aag cct aaa ttt gtg tca gtc act tac ggt gca aat tcg gga gaa 192
 Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu
 50 55 60
 cgt gac cgc act cac ggc att gtg aaa gcc att aaa caa gaa act ggc 240
 Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly
 65 70 75 80
 tta gaa gcc gca cca cat tta act gga att gat gcc aca cct gaa gaa 288
 Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu
 85 90 95
 tta aaa caa att gcg aga gat tat tgg gat agt ggt att cgc cgt att 336
 eu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile
 100 105 110
 gtt gcg tta cgc ggt gac gaa cct aaa ggt tac gcg aaa aaa cca ttt 384
 Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe
 115 120 125
 tat gcg tca gat ctt gtg gaa tta ctc cgt tct gtc gct gat ttt gat 432
 Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp
 130 135 140
 att tct gta gcc gct tat ccc gaa gtt cat cca gaa gca aaa tcc gca 480
 Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160
 caa gca gac tta att aat tta aaa cgt aaa att gat gca ggt gca aac 528
 Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175
 cac gtc att aca caa ttt ttc ttt gat att gaa aac tac cta cgt ttt 576
 His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe
 180 185 190

cgt gat cgt tgt gca tca att ggt att gat act gaa atc gta ccc ggt	624
Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly	
195 200 205	
att tta cct gtt act aat ttt aaa caa ctc caa aaa atg gca tca ttc	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe	
210 215 220	
act aat gtg aaa att cca gcg tgg tta gtt aaa gcc tat gat ggt ttg	720
Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu	
225 230 235 240	
gat aat gat cca act aca cgt aat ctt gtg gca gca agt gtt gca atg	768
Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met	
245 250 255	
gat atg gta aaa att tta tct cgc gaa ggc gtg aat gac ttc cac ttt	816
Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe	
260 265 270	
t aca tta aat cgt agt gaa tta act tat gct atc tgt cat atg tta	864
Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu	
275 280 285	
ggt gta aga cct taa	879
Gly Val Arg Pro	
290	
<210> 38	
<211> 292	
<212> PRT	
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<400> 38	
Met Ser Tyr Ala Lys Glu Ile Asp Thr Leu Asn Gln His Ile Ala Asp	
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Phe Asn Lys Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn	
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Glu Lys Met Glu Thr Leu Leu Trp Asp Ser Ile His Arg Leu Lys Val	
35 40 45	
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
Arg Asp Arg Thr His Gly Ile Val Lys Ala Ile Lys Gln Glu Thr Gly	
65 70 75 80	
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Pro Glu Glu	
85 90 95	
Leu Lys Gln Ile Ala Arg Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Ala Lys Lys Pro Phe	
115 120 125	
Tyr Ala Ser Asp Leu Val Glu Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	

Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala
 145 150 155 160
 Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175
 His Val Ile Thr Gln Phe Phe Phe Asp Ile Glu Asn Tyr Leu Arg Phe
 180 185 190
 Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Thr Glu Ile Val Pro Gly
 195 200 205
 Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ser Phe
 210 215 220
 Thr Asn Val Lys Ile Pro Ala Trp Leu Val Lys Ala Tyr Asp Gly Leu
 225 230 235 240
 Asp Asn Asp Pro Thr Thr Arg Asn Leu Val Ala Ala Ser Val Ala Met
 245 250 255
 Asp Met Val Lys Ile Leu Ser Arg Glu Gly Val Asn Asp Phe His Phe
 260 265 270
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Met Leu
 275 280 285
 Gly Val Arg Pro
 290

<210> 39
 <211> 945
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1) .. (942)
 <223> RCO02274

400> 39
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 1 5 10 15
 gcc gag cgg acc gcc cgt ccg cgc gtg tcg ttc gag ttc ttc ccg ccc 96
 Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro
 20 25 30
 aag act ccg cag atg gaa gag agc ctg tgg cag gcg atc aca cgc ctg 144
 Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
 35 40 45
 gcg ccg ctg gat ccg gcc ttc gtc tcg gtg acc tat gcc gcg gcc gcc 192
 Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly
 50 55 60
 tcc acc cgc gag cgc acc cac cgc acc gtc aag cgg atc ctg gac gag 240
 Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu
 65 70 75 80

acc agc ctc aag ccc gcc gcg cac ctg acc tgc gtc ggc gcc agt cgc	288
Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg	
85 90 95	
gaa gag gtc gat gag gtc att cgc gag tac tgg gag acc ggg gtc cgt	336
Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg	
100 105 110	
cac atc gtt tgc ctg cgg ggc gat ccg ccg ccc ggc gag ggc ggc atc	384
His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile	
115 120 125	
ggc ggg gtc tat gtg ccg cgc gcc gac ggc tac gcc aac gcc aca gag	432
Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu	
130 135 140	
ttg acc aag gcc gtg cgc gcg atc gcg ccg ttc gag gtg ctg gtc ggg	480
Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly	
145 150 155 160	
ctc tat ccc gag aag cat ccc gag agc ccc tgc ttg gag cac gac atc	528
1 Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile	
165 170 175	
gac gtc ttg aag cag aag gtc gac gcc ggc gcg acg ctg ggg atc agc	576
Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser	
180 185 190	
cag ttc ttc ttc gac ctc gac gcc ttc ctg cgc ttc gtc gac aag gtg	624
Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val	
195 200 205	
cgc gcg gcg ggc atc acc att ccg atc gtg ccg ggg atc atg ccg gtg	672
Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val	
210 215 220	
acc aat ttc gcg ggc ttg aag aag atg gcc gcc gcc tgc cag acg gcc	720
Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala	
225 230 235 240	
atc ccg tcc tgg ctg ggg aac ctg ttc gac ggg ctg gag aac gac gcg	768
1le Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala	
245 250 255	
gag acc cgc cgc ctg atc gcc tgt tgc gtg gcc gcc gag atg tgc gcc	816
Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala	
260 265 270	
aag ctg cag gaa cag ggt ttc gag gac ttc cac ttc tac acc ctg aac	864
Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn	
275 280 285	
cgg gcc gat ctc gtt tac gcc atc tgc cgt gtg ctg ggc gtg cgc gag	912
Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu	
290 295 300	
atc tgc ccc gcc gct tgc gag gtc gcc gca tga	945
Ile Ser Pro Ala Ala Ser Glu Val Ala Ala	
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<210> 40

<211> 314

<212> PRT

<213> *Caulobacter crescentus*

<400> 40

Met Thr Leu Pro Pro Thr Arg Arg Val Ile Gly Pro Val Ala Arg Ala
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Gly Glu Arg Thr Gly Arg Pro Arg Val Ser Phe Glu Phe Phe Pro Pro
20 25 30
Lys Thr Pro Gln Met Glu Glu Ser Leu Trp Gln Ala Ile Thr Arg Leu
35 40 45
Ala Pro Leu Asp Pro Ala Phe Val Ser Val Thr Tyr Gly Ala Gly Gly
50 55 60
Ser Thr Arg Glu Arg Thr His Arg Thr Val Lys Arg Ile Leu Asp Glu
65 70 75 80
Thr Ser Leu Lys Pro Ala Ala His Leu Thr Cys Val Gly Ala Ser Arg
85 90 95
Glu Glu Val Asp Glu Val Ile Arg Glu Tyr Trp Glu Thr Gly Val Arg
100 105 110
His Ile Val Ser Leu Arg Gly Asp Pro Pro Pro Gly Glu Gly Gly Ile
115 120 125
Gly Gly Val Tyr Val Pro Arg Ala Asp Gly Tyr Ala Asn Ala Thr Glu
130 135 140
Leu Thr Lys Ala Val Arg Ala Ile Ala Pro Phe Glu Val Leu Val Gly
145 150 155 160
Val Tyr Pro Glu Lys His Pro Glu Ser Pro Ser Leu Glu His Asp Ile
165 170 175
Asp Val Leu Lys Gln Lys Val Asp Ala Gly Ala Thr Leu Gly Ile Ser
180 185 190
Gln Phe Phe Phe Asp Leu Asp Ala Phe Leu Arg Phe Val Asp Lys Val
195 200 205
Arg Ala Ala Gly Ile Thr Ile Pro Ile Val Pro Gly Ile Met Pro Val
210 215 220
Thr Asn Phe Ala Gly Leu Lys Lys Met Ala Ala Ala Cys Gln Thr Ala
225 230 235 240
Ile Pro Ser Trp Leu Gly Asn Leu Phe Asp Gly Leu Glu Asn Asp Ala
245 250 255
Glu Thr Arg Arg Leu Ile Ala Cys Ser Val Ala Ala Glu Met Cys Ala
260 265 270
Lys Leu Gln Glu Gln Gly Phe Glu Asp Phe His Phe Tyr Thr Leu Asn
275 280 285
Arg Ala Asp Leu Val Tyr Ala Ile Cys Arg Val Leu Gly Val Arg Glu
290 295 300
Ile Ser Pro Ala Ala Ser Glu Val Ala Ala
305 310

<210> 41
 <211> 885
 <212> DNA
 <213> Actinobacillus actinomycetemcomitans

<220>
 <221> CDS
 <222> (1)..(882)

<223> RAB00260

<400> 41

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tta aac ggc aaa att aat gtc tct ttt gaa ttt ttc ccg ccg aaa agt	96
Leu Asn Gly Lys Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Ser	
20 25 30	
aaa atg gaa aat ctt ctg tgg gaa tcc atc cat cgc tta aaa gtg	144
Glu Lys Met Glu Asn Leu Leu Trp Glu Ser Ile His Arg Leu Lys Val	
35 40 45	
cta aaa ccg aaa ttt gta tcc gtg act tac ggc gcc aat tcc ggc gag	192
Leu Lys Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgt gaa cgc act cac ggg gtg gtg aaa cgc att aag cag gaa acc ggt	240
Arg Glu Arg Thr His Gly Val Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
ctg gaa gct gcg ccg cat tta acc ggt att gac gct acc tcg gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Thr Ser Asp Glu	
85 90 95	
ttg cgt cgc att gcc aaa ggt tat tgg gat agc ggc att cgt cgc att	336
Leu Arg Arg Ile Ala Lys Gly Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
tg gca ctg cgc ggt gac gag ccg aaa ggc tac gag aaa aaa cca ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Lys Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tat gcc gcc gat tta gta gca tta tta cgt gac gta tca gat ttt gat	432
Tyr Ala Ala Asp Leu Val Ala Leu Leu Arg Asp Val Ser Asp Phe Asp	
130 135 140	
att tcc gtg gcg gca tac cct gag gtt cat ccg gaa gcc aaa tcg gcg	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
caa gcg gat tta att aat tta aaa cgt aaa att gat gcc ggt gcc aat	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cat gtg atc aca caa ttc ttt ttc gat att gac agc tat ctg cgg ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe	
180 185 190	
cgc gat cgc tgc gcg tct atc ggt att gat gca gaa atc gtg ccg ggg	624

Arg	Asp	Arg	Cys	Ala	Ser	Ile	Gly	Ile	Asp	Ala	Glu	Ile	Val	Pro	Gly	
	195						200					205				
att	ctg	ccg	gtg	acc	aac	ttc	aaa	caa	tta	caa	aaa	atg	gca	gca	atc	672
Ile	Leu	Pro	Val	Thr	Asn	Phe	Lys	Gln	Leu	Gln	Lys	Met	Ala	Ala	Ile	
	210					215					220					
act	aat	gtg	aaa	att	cca	gct	tgg	atg	agc	aaa	atg	tat	gaa	ggc	ttg	720
Thr	Asn	Val	Lys	Ile	Pro	Ala	Trp	Met	Ser	Lys	Met	Tyr	Glu	Gly	Leu	
	225				230					235					240	
gat	gat	gac	caa	acc	acc	cgc	aat	ctg	gtg	gcg	gcg	agc	atc	gcc	atg	768
Asp	Asp	Asp	Gln	Thr	Thr	Arg	Asn	Leu	Val	Ala	Ala	Ser	Ile	Ala	Met	
				245					250					255		
gac	atg	gtg	cgt	gta	ctg	tcc	cgc	gaa	ggg	gta	aaa	gac	ttt	cat	ttc	816
Asp	Met	Val	Arg	Val	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe	
			260					265					270			
tac	acc	ctg	aat	cgc	agt	gaa	ctc	acc	tat	gct	att	tgc	cac	acg	tta	864
Tyr	Thr	Leu	Asn	Arg	Ser	Glu	Leu	Thr	Tyr	Ala	Ile	Cys	His	Thr	Leu	
		275				280						285				
ggc	att	cgt	ccg	agt	ttg	taa										885
Gly	Ile	Arg	Pro	Ser	Leu											
	290															

<210> 42
 <211> 294
 <212> PRT
 <213> Actinobacillus actinomycetemcomitans

<400> 42

Met	Ser	Tyr	Ala	Lys	Glu	Ile	Asp	Asn	Leu	Asn	Gln	His	Leu	Ala	Asp	
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Leu	Asn	Gly	Lys	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Lys	Ser	
		20						25					30			
Glu	Lys	Met	Glu	Asn	Leu	Leu	Trp	Glu	Ser	Ile	His	Arg	Leu	Lys	Val	
		35					40					45				
Leu	Lys	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	Gly	Glu	
	50					55					60					
Arg	Glu	Arg	Thr	His	Gly	Val	Val	Lys	Arg	Ile	Lys	Gln	Glu	Thr	Gly	
	65				70					75					80	
Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Gly	Ile	Asp	Ala	Thr	Ser	Asp	Glu	
				85					90					95		
Leu	Arg	Arg	Ile	Ala	Lys	Gly	Tyr	Trp	Asp	Ser	Gly	Ile	Arg	Arg	Ile	
			100					105					110			
Val	Ala	Leu	Arg	Gly	Asp	Glu	Pro	Lys	Gly	Tyr	Glu	Lys	Lys	Pro	Phe	
		115					120					125				
Tyr	Ala	Ala	Asp	Leu	Val	Ala	Leu	Leu	Arg	Asp	Val	Ser	Asp	Phe	Asp	
	130					135					140					
Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys	Ser	Ala	
	145				150					155					160	

Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn
 165 170 175
 His Val Ile Thr Gln Phe Phe Phe Asp Ile Asp Ser Tyr Leu Arg Phe
 180 185 190
 Arg Asp Arg Cys Ala Ser Ile Gly Ile Asp Ala Glu Ile Val Pro Gly
 195 200 205
 Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gln Lys Met Ala Ala Ile
 210 215 220
 Thr Asn Val Lys Ile Pro Ala Trp Met Ser Lys Met Tyr Glu Gly Leu
 225 230 235 240
 Asp Asp Asp Gln Thr Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Met
 245 250 255
 Asp Met Val Arg Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270
 Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Thr Leu
 275 280 285
 Gly Ile Arg Pro Ser Leu
 290

<210> 43
 <211> 867
 <212> DNA
 <213> Rhodobacter

<220>
 <221> CDS
 <222> (1) .. (864)
 <223> RRC03981

<400> 43

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 1 5 10 15
 gac gcc tcg ttc cgg ctg tgg gag acg gcg cag gtt ctg gcg ccg ctc 96
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu
 20 25 30
 aag ccc ggc ttc gtc tcg gtc acc tat ggc gcg ggc ggc acc acc cgc 144
 Lys Pro Gly Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Thr Thr Arg
 35 40 45
 aag ctg acg cat gag gcc gtg gcg gcg atc cac aag aat tac ggc ctg 192
 Lys Leu Thr His Glu Ala Val Ala Ala Ile His Lys Asn Tyr Gly Leu
 50 55 60
 aac gtc gcc gcg cat ctg acc tgc gtc gat gcg acc cgg gcc gaa acg 240
 Asn Val Ala Ala His Leu Thr Cys Val Asp Ala Thr Arg Ala Glu Thr
 65 70 75 80
 caa gag atc atc gac gcc tat gcc gag gct ggc gtc acc gag att gtc 288
 Gln Glu Ile Ile Asp Ala Tyr Ala Glu Ala Gly Val Thr Glu Ile Val
 85 90 95

gcg ctg cgc ggt gat ccg ccg aaa ggc gcc gcc cgc ttc acg ccg cat	336
Ala Leu Arg Gly Asp Pro Pro Lys Gly Ala Ala Arg Phe Thr Pro His	
100 105 110	
ccg gac ggg ttt gcc tcc tgc gtg gac ctc atc gaa tgg ctg gcg cgg	384
Pro Asp Gly Phe Ala Ser Ser Val Asp Leu Ile Glu Trp Leu Ala Arg	
115 120 125	
gac ggc cgc ttc acg ctg cgc tgc ggc gcc tat ccg gaa ccg cat ccg	432
Asp Gly Arg Phe Thr Leu Arg Cys Gly Ala Tyr Pro Glu Pro His Pro	
130 135 140	
gaa gcc gcc gac acg ctg gcc gac gtg cgc tgg ctg aaa cgc aaa tgc	480
Glu Ala Ala Asp Thr Leu Ala Asp Val Arg Trp Leu Lys Arg Lys Cys	
145 150 155 160	
gag gcg ggg gcg acc tgc gcg atc acg caa ttc ttc ttt gaa gcc gag	528
Glu Ala Gly Ala Thr Ser Ala Ile Thr Gln Phe Phe Phe Glu Ala Glu	
165 170 175	
ccg ttc ttc cgc ttc cgc gac gcc tgc gtg aag gaa ggg atc acc gcc	576
Arg Phe Phe Arg Phe Arg Asp Ala Cys Val Lys Glu Gly Ile Thr Ala	
180 185 190	
aag atc atc ccg ggc atc ctg ccg atc cag tcc tgg aaa ggc gcc aag	624
Lys Ile Ile Pro Gly Ile Leu Pro Ile Gln Ser Trp Lys Gly Ala Lys	
195 200 205	
agc ttt gcg cag cgc tgc ggc acc tgc atc ccg acc tgg gtc gaa gag	672
Ser Phe Ala Gln Arg Cys Gly Thr Ser Ile Pro Thr Trp Val Glu Glu	
210 215 220	
gcc ttt gac cat gcg atc cgc gac gac cgc gaa cag ctg ctg gcc acg	720
Ala Phe Asp His Ala Ile Arg Asp Asp Arg Glu Gln Leu Leu Ala Thr	
225 230 235 240	
gcg ctg tgc acg gag ctc tgc gac aac ctg atc gcg ggc ggg gtg gag	768
Ala Leu Cys Thr Glu Leu Cys Asp Asn Leu Ile Ala Gly Gly Val Glu	
245 250 255	
at ctg cat ttc tac acg ctg aac cgc ccg cag atg acc cgc gat gtc	816
Asp Leu His Phe Tyr Thr Leu Asn Arg Pro Gln Met Thr Arg Asp Val	
260 265 270	
tgc cat gcg ctg ggc gtc aac ccg ggt gtg gtg ctg gaa aac gtc gcc	864
Cys His Ala Leu Gly Val Asn Pro Gly Val Val Leu Glu Asn Val Ala	
275 280 285	
tga	867

<210> 44
 <211> 288
 <212> PRT
 <213> Rhodobacter

<400> 44
 Met Thr Thr Pro His Val Ser Phe Glu Phe Phe Pro Pro Gln Thr Leu
 1 5 10 15
 Asp Ala Ser Phe Arg Leu Trp Glu Thr Ala Gln Val Leu Ala Pro Leu
 20 25 30

Lys	Pro	Gly	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Gly	Gly	Thr	Thr	Arg	35	40	45	
Lys	Leu	Thr	His	Glu	Ala	Val	Ala	Ala	Ile	His	Lys	Asn	Tyr	Gly	Leu	50	55	60	
Asn	Val	Ala	Ala	His	Leu	Thr	Cys	Val	Asp	Ala	Thr	Arg	Ala	Glu	Thr	65	70	75	80
Gln	Glu	Ile	Ile	Asp	Ala	Tyr	Ala	Glu	Ala	Gly	Val	Thr	Glu	Ile	Val	85	90	95	
Ala	Leu	Arg	Gly	Asp	Pro	Pro	Lys	Gly	Ala	Ala	Arg	Phe	Thr	Pro	His	100	105	110	
Pro	Asp	Gly	Phe	Ala	Ser	Ser	Val	Asp	Leu	Ile	Glu	Trp	Leu	Ala	Arg	115	120	125	
Asp	Gly	Arg	Phe	Thr	Leu	Arg	Cys	Gly	Ala	Tyr	Pro	Glu	Pro	His	Pro	130	135	140	
Leu	Ala	Ala	Asp	Thr	Leu	Ala	Asp	Val	Arg	Trp	Leu	Lys	Arg	Lys	Cys	145	150	155	160
Glu	Ala	Gly	Ala	Thr	Ser	Ala	Ile	Thr	Gln	Phe	Phe	Phe	Glu	Ala	Glu	165	170	175	
Thr	Phe	Phe	Arg	Phe	Arg	Asp	Ala	Cys	Val	Lys	Glu	Gly	Ile	Thr	Ala	180	185	190	
Lys	Ile	Ile	Pro	Gly	Ile	Leu	Pro	Ile	Gln	Ser	Trp	Lys	Gly	Ala	Lys	195	200	205	
Ser	Phe	Ala	Gln	Arg	Cys	Gly	Thr	Ser	Ile	Pro	Thr	Trp	Val	Glu	Glu	210	215	220	
Ala	Phe	Asp	His	Ala	Ile	Arg	Asp	Asp	Arg	Glu	Gln	Leu	Leu	Ala	Thr	225	230	235	240
Ala	Leu	Cys	Thr	Glu	Leu	Cys	Asp	Asn	Leu	Ile	Ala	Gly	Gly	Val	Glu	245	250	255	
Asp	Leu	His	Phe	Tyr	Thr	Leu	Asn	Arg	Pro	Gln	Met	Thr	Arg	Asp	Val	260	265	270	
Cys	His	Ala	Leu	Gly	Val	Asn	Pro	Gly	Val	Val	Leu	Glu	Asn	Val	Ala	275	280	285	

<210> 45

<211> 879

<212> DNA

<213> Neisseria meningitidis ser. A

<220>

<221> CDS

<222> (1)..(876)

<223> RNM00812

<400> 45

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1 5 10 15	
ttg aaa ggc gac atc aac gtt tcg ttt gaa ttt ttt cca ccg aaa aac	96
Leu Lys Gly Asp Ile Asn Val Ser Phe Glu Phe Phe Pro Pro Lys Asn	
20 25 30	
gag caa atg gaa acg atg ctg tgg gat tcc atc cac cgt ctg caa acc	144
Glu Gln Met Glu Thr Met Leu Trp Asp Ser Ile His Arg Leu Gln Thr	
35 40 45	
ctg cat ccc aag ttc gta tcc gta acc tac ggc gca aac tcc ggc gaa	192
Leu His Pro Lys Phe Val Ser Val Thr Tyr Gly Ala Asn Ser Gly Glu	
50 55 60	
cgc gac cgc acg cac ggc atc gtc aaa cgc atc aaa cag gaa acc ggc	240
Arg Asp Arg Thr His Gly Ile Val Lys Arg Ile Lys Gln Glu Thr Gly	
65 70 75 80	
g gaa gca gca ccg cac ctg acc ggc atc gac gca tcc ccc gac gaa	288
Leu Glu Ala Ala Pro His Leu Thr Gly Ile Asp Ala Ser Pro Asp Glu	
85 90 95	
ttg cgc caa atc gcc aaa gac tat tgg gac agc ggc atc cgc cgc att	336
Leu Arg Gln Ile Ala Lys Asp Tyr Trp Asp Ser Gly Ile Arg Arg Ile	
100 105 110	
gtc gcc ctg cgt ggc gac gag ccg ccc ggt tat gag aaa aaa ccg ttt	384
Val Ala Leu Arg Gly Asp Glu Pro Pro Gly Tyr Glu Lys Lys Pro Phe	
115 120 125	
tac gcc gaa gac ttg gtt aag cta tta cgc tcc gtc gcc gac ttc gac	432
Tyr Ala Glu Asp Leu Val Lys Leu Leu Arg Ser Val Ala Asp Phe Asp	
130 135 140	
atc tct gtg gcg gca tat ccc gaa gtg cat ccc gaa gcc aaa tcc gca	480
Ile Ser Val Ala Ala Tyr Pro Glu Val His Pro Glu Ala Lys Ser Ala	
145 150 155 160	
aa gcc gat ctg att aat ctg aag cgc aaa atc gat gcg ggt gca aac	528
Gln Ala Asp Leu Ile Asn Leu Lys Arg Lys Ile Asp Ala Gly Ala Asn	
165 170 175	
cac gtc atc acc caa ttt ttc ttt gac gta gaa cgc tac ctg cgc ttc	576
His Val Ile Thr Gln Phe Phe Phe Asp Val Glu Arg Tyr Leu Arg Phe	
180 185 190	
cgc gac cgc tgc gtg atg ttg ggt atc gat gtg gaa atc gtc cct ggt	624
Arg Asp Arg Cys Val Met Leu Gly Ile Asp Val Glu Ile Val Pro Gly	
195 200 205	
att ttg cct gtt acc aac ttc aag cag ctc ggc aaa atg gcg caa gta	672
Ile Leu Pro Val Thr Asn Phe Lys Gln Leu Gly Lys Met Ala Gln Val	
210 215 220	
acc aac gtc aaa atc cca agc tgg ctg tcg caa atg tat gaa ggt ttg	720
Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu	
225 230 235 240	
gac gac gac caa ggc acg cgc aac ctc gtc gcc gcc agt atc gcc atc	768
Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile	

245										250					255					
gat	atg	gtc	aaa	gtc	ctg	tcc	cgc	gaa	ggc	gtg	aaa	gat	ttc	cac	ttc	816				
Asp	Met	Val	Lys	Val	Leu	Ser	Arg	Glu	Gly	Val	Lys	Asp	Phe	His	Phe					
			260				265						270							
tac	acg	ctc	aac	cgc	agc	gag	ctg	act	tac	gcc	atc	tgc	cat	att	tta	864				
Tyr	Thr	Leu	Asn	Arg	Ser	Glu	Leu	Thr	Tyr	Ala	Ile	Cys	His	Ile	Leu					
			275				280						285							
ggc	gtg	cgc	cct	taa											879					
Gly	Val	Arg	Pro																	
				290																

<210> 46
 <211> 292
 <212> PRT
 <213> Neisseria meningitidis ser. A

400> 46

t	Asn	Tyr	Ala	Lys	Glu	Ile	Asn	Ala	Leu	Asn	Asn	Ser	Leu	Ser	Asp
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Leu	Lys	Gly	Asp	Ile	Asn	Val	Ser	Phe	Glu	Phe	Phe	Pro	Pro	Lys	Asn
			20					25					30		
Glu	Gln	Met	Glu	Thr	Met	Leu	Trp	Asp	Ser	Ile	His	Arg	Leu	Gln	Thr
		35					40					45			
Leu	His	Pro	Lys	Phe	Val	Ser	Val	Thr	Tyr	Gly	Ala	Asn	Ser	Gly	Glu
	50					55					60				
Arg	Asp	Arg	Thr	His	Gly	Ile	Val	Lys	Arg	Ile	Lys	Gln	Glu	Thr	Gly
	65				70					75					80
Leu	Glu	Ala	Ala	Pro	His	Leu	Thr	Gly	Ile	Asp	Ala	Ser	Pro	Asp	Glu
				85					90					95	
Leu	Arg	Gln	Ile	Ala	Lys	Asp	Tyr	Trp	Asp	Ser	Gly	Ile	Arg	Arg	Ile
		100						105					110		
al	Ala	Leu	Arg	Gly	Asp	Glu	Pro	Pro	Gly	Tyr	Glu	Lys	Lys	Pro	Phe
		115					120					125			
Tyr	Ala	Glu	Asp	Leu	Val	Lys	Leu	Leu	Arg	Ser	Val	Ala	Asp	Phe	Asp
		130				135					140				
Ile	Ser	Val	Ala	Ala	Tyr	Pro	Glu	Val	His	Pro	Glu	Ala	Lys	Ser	Ala
	145				150					155					160
Gln	Ala	Asp	Leu	Ile	Asn	Leu	Lys	Arg	Lys	Ile	Asp	Ala	Gly	Ala	Asn
			165						170					175	
His	Val	Ile	Thr	Gln	Phe	Phe	Phe	Asp	Val	Glu	Arg	Tyr	Leu	Arg	Phe
		180						185					190		
Arg	Asp	Arg	Cys	Val	Met	Leu	Gly	Ile	Asp	Val	Glu	Ile	Val	Pro	Gly
		195					200					205			
Ile	Leu	Pro	Val	Thr	Asn	Phe	Lys	Gln	Leu	Gly	Lys	Met	Ala	Gln	Val
		210				215					220				

Thr Asn Val Lys Ile Pro Ser Trp Leu Ser Gln Met Tyr Glu Gly Leu
 225 230 235 240
 Asp Asp Asp Gln Gly Thr Arg Asn Leu Val Ala Ala Ser Ile Ala Ile
 245 250 255
 Asp Met Val Lys Val Leu Ser Arg Glu Gly Val Lys Asp Phe His Phe
 260 265 270
 Tyr Thr Leu Asn Arg Ser Glu Leu Thr Tyr Ala Ile Cys His Ile Leu
 275 280 285
 Gly Val Arg Pro
 290

<210> 47
 <211> 849
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(846)
 <223> RCJ02911

<400> 47
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 Met Cys Ser Phe Ser Phe Glu Val Phe Pro Pro Arg Lys Asp Glu Asn
 1 5 10 15
 atc aaa aat ctt cat gct atc tta gat gat tta ggg caa tta agc cct 96
 Ile Lys Asn Leu His Ala Ile Leu Asp Asp Leu Gly Gln Leu Ser Pro
 20 25 30
 aat ttt atc agc gta acc ttt gga gct gga ggc tct att aac tca caa 144
 Asn Phe Ile Ser Val Thr Phe Gly Ala Gly Gly Ser Ile Asn Ser Gln
 35 40 45
 aat act tta gaa gtt gca agc tta atc cag gaa gaa tat caa att cct 192
 Asn Thr Leu Glu Val Ala Ser Leu Ile Gln Glu Glu Tyr Gln Ile Pro
 50 55 60
 agc ata gta cat tta cct tgc atc cat tct agt aaa gaa aaa atc act 240
 Ser Ile Val His Leu Pro Cys Ile His Ser Ser Lys Glu Lys Ile Thr
 65 70 75 80
 cag ata ctt caa aaa tgc aaa gaa aaa aat ctt aat caa att ctt gcc 288
 Gln Ile Leu Gln Lys Cys Lys Glu Lys Asn Leu Asn Gln Ile Leu Ala
 85 90 95
 cta aga ggc gat ata tgt gaa aat tta aaa aaa agc aaa gat ttt tct 336
 Leu Arg Gly Asp Ile Cys Glu Asn Leu Lys Lys Ser Lys Asp Phe Ser
 100 105 110
 tat gct agt gat tta att tct ttt ata aaa aaa caa gaa tac ttt gaa 384
 Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
 115 120 125
 att tat gcc gca tgc tat ccc gaa aaa cat aat gaa tct aaa aat ttc 432
 Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
 130 135 140

[illegible]

100

105

110

Tyr Ala Ser Asp Leu Ile Ser Phe Ile Lys Lys Gln Glu Tyr Phe Glu
115 120 125

Ile Tyr Ala Ala Cys Tyr Pro Glu Lys His Asn Glu Ser Lys Asn Phe
130 135 140

Ile Glu Asp Ile His His Leu Lys Thr Lys Val Asn Ala Gly Thr Asp
145 150 155 160

Lys Leu Ile Thr Gln Leu Phe Tyr Asp Asn Glu Asp Phe Tyr Thr Phe
165 170 175

Lys Gln Asn Cys Ala Leu Ala Asp Ile Asp Ile Pro Ile Tyr Ala Gly
180 185 190

Ile Met Pro Ile Thr Asn Lys Arg Gln Val Leu Lys Ile Ser Gln Leu
195 200 205

Cys Gly Ala Lys Ile Pro Pro Lys Phe Val Lys Ile Leu Glu Lys Tyr
210 215 220

Asn Asn Thr Leu Ala Leu Glu Asp Ala Gly Ile Ala Tyr Ala Cys
225 230 235 240

Asp Gln Ile Val Asp Leu Ile Thr Ser Gly Val Asp Gly Ile His Leu
245 250 255

Tyr Thr Met Asn Lys Ser Lys Ala Ala Ile Lys Ile Tyr Glu Ala Val
260 265 270

Lys His Leu Leu Lys Glu Glu Leu His Ala
275 280

<210> 49

<211> 852

<212> DNA

<213> Lactococcus lactis

<220>

<221> CDS

<222> (1) .. (849)

<223> AAK05352

<400> 49

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Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr
1 5 10 15

act caa att gga agt acc aac ttg gta aag acc ttg gat agc cta aga 96
Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg
20 25 30

act ctc tcg cca gat ttt atc agt gta act tgt agt aac aat aat tat 144
Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
35 40 45

gat aat att gga gat aca act ata aag ttt gct gat tat gta aac aat 192
Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn
50 55 60

aca cta gat att cca gcg gtt gct cat tta cct gcc gct tat tta gat	240
Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp	
65 70 75 80	
aaa gct caa gtg atc gaa att ttg gaa cgg tta aaa gat aaa caa atc	288
Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile	
85 90 95	
aaa aaa att ctt gct tta aga ggt gat atc agc gat gaa ccg atg aaa	336
Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys	
100 105 110	
gat gat ttt aaa ttt gca agt gat ttg gtt aaa ttt atc aaa gat tat	384
Asp Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr	
115 120 125	
gat gat agt ttt gaa gtt tta ggt gct tgc tac ccc gat att cat ccc	432
Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro	
130 135 140	
gaa tca gta aat cga gtg agt gat ttt cat tat ctg aaa gaa aaa gta	480
Val Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val	
150 155 160	
gat gct ggt tgt gac aga tta atc acg caa cta ttt ttt gat aat gat	528
Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp	
165 170 175	
agt ttc tat gat ttt caa gaa cga tgc gca att gct gag ata aat act	576
Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr	
180 185 190	
ccg ata ttc gcc gga ata atg cca gta atc aat cga aat caa att ctt	624
Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu	
195 200 205	
cgt cta tta aaa aat tgt aat acg cca tta cca gca aaa ttc att aga	672
Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg	
210 215 220	
ata ctc gaa aaa tat gaa cat aat ctt atc gct tta agg gat gct gga	720
Ile Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly	
230 235 240	
att gct tac gcc atc gat caa atc gtt gat tta gta aca gag gat gtt	768
Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val	
245 250 255	
gct gga att cac ctc tat acg atg aat aat gca aat acg gca cac tcc	816
Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser	
260 265 270	
atc cat gct tca att tct tct tta ttt acc ttt tga	852
Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe	
275 280	

<210> 50

<211> 283

<212> PRT

<213> Lactococcus lactis.

<400> 50

Met Thr Ser Asn Ser Lys Ile Leu Ser Phe Glu Val Phe Pro Pro Thr
1 5 10 15

Thr Gln Ile Gly Ser Thr Asn Leu Val Lys Thr Leu Asp Ser Leu Arg
20 25 30

Thr Leu Ser Pro Asp Phe Ile Ser Val Thr Cys Ser Asn Asn Asn Tyr
35 40 45

Asp Asn Ile Gly Asp Thr Thr Ile Lys Phe Ala Asp Tyr Val Asn Asn
50 55 60

Thr Leu Asp Ile Pro Ala Val Ala His Leu Pro Ala Ala Tyr Leu Asp
65 70 75 80

Lys Ala Gln Val Ile Glu Ile Leu Glu Arg Leu Lys Asp Lys Gln Ile
85 90 95

Lys Lys Ile Leu Ala Leu Arg Gly Asp Ile Ser Asp Glu Pro Met Lys
100 105 110

Asp Phe Lys Phe Ala Ser Asp Leu Val Lys Phe Ile Lys Asp Tyr
115 120 125

Asp Asp Ser Phe Glu Val Leu Gly Ala Cys Tyr Pro Asp Ile His Pro
130 135 140

Glu Ser Val Asn Arg Val Ser Asp Phe His Tyr Leu Lys Glu Lys Val
145 150 155 160

Asp Ala Gly Cys Asp Arg Leu Ile Thr Gln Leu Phe Phe Asp Asn Asp
165 170 175

Ser Phe Tyr Asp Phe Gln Glu Arg Cys Ala Ile Ala Glu Ile Asn Thr
180 185 190

Pro Ile Phe Ala Gly Ile Met Pro Val Ile Asn Arg Asn Gln Ile Leu
195 200 205

Arg Leu Leu Lys Asn Cys Asn Thr Pro Leu Pro Ala Lys Phe Ile Arg
210 215 220

Leu Glu Lys Tyr Glu His Asn Leu Ile Ala Leu Arg Asp Ala Gly
225 230 235 240

Ile Ala Tyr Ala Ile Asp Gln Ile Val Asp Leu Val Thr Glu Asp Val
245 250 255

Ala Gly Ile His Leu Tyr Thr Met Asn Asn Ala Asn Thr Ala His Ser
260 265 270

Ile His Ala Ser Ile Ser Ser Leu Phe Thr Phe
275 280

<210> 51

<211> 891

<212> DNA

<213> *Prochlorococcus maritima*

<220>

<221> CDS

M/43126

MetE

<222> (1)..(888)

<223> RCK01602

<400> 51

ttg aaa tca aaa ctt cag caa act tta gaa aag aat tca aaa gta att 48
Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile
1 5 10 15

aca gca gaa tta atg ccg cca aga gga gga gac ccc gta aga tct ctt 96
Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
20 25 30

aaa ata gca caa ctc ttg aga aat aag gtg cat gca gtt aat att aca 144
Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
35 40 45

gac gga agt aga gca ata atg aga atg tgt agt tta gca atg tct aaa 192
Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
50 55 60

cta tta cta gac aat ggg ata gaa cct ata atg cag atc tca tgt aga 240
Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
70 75 80

gat cgt aat aaa att gct tta caa tca gat att ctt gga gca aat gcc 288
Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
85 90 95

tta gga att aaa aat att tta tgc att aca gga gat tct gta aaa gcc 336
Leu Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
100 105 110

gga gat cag caa gaa aca aaa gcc gtt cat gaa ttt gag gca gta aga 384
Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
115 120 125

tta tta aaa caa att caa tca ttc aat caa gga att gat cct act ttt 432
Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
130 135 140

gaa caa ctt cca gac aaa agg act gaa att ttc tca ggt gcg gca gta 480
Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
150 155 160

gat cca agt tgt cga aat caa aga agt tta aaa agt aga aca att aaa 528
Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
165 170 175

aaa aaa gag gcc ggt gca aat ttc tta caa act caa ata gtt atg gat 576
Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
180 185 190

aga aaa tgt tta gca gac ttt tgc aac gaa atc agt aat cca ctt gag 624
Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
195 200 205

ata cca gtt att gca gga gta ttt ctt tta aaa tca tat aaa aat gct 672
Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
210 215 220

ctt ttc ata aat aaa ttt gta cct gga gcg aat att cct gaa aat gtt 720
Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
225 230 235 240

tta aat cgt ctc aaa gat gca aaa aat cca ctt caa gaa gga ata tta 768
 Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255

att gct tca gag caa gct caa gat ttt att aat att gca gat gga att 816
 Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270

cat ctt atg gca gtc aaa tca gaa cat ctt atc cca gag ata ctt gaa 864
 His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285

aaa gct ggt ctc aat ctg gaa tgt taa 891
 Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 52

<211> 296

<212> PRT

13> *Prochlorococcus maritima*

0> 52

Leu Lys Ser Lys Leu Gln Gln Thr Leu Glu Lys Asn Ser Lys Val Ile
 1 5 10 15

Thr Ala Glu Leu Met Pro Pro Arg Gly Gly Asp Pro Val Arg Ser Leu
 20 25 30

Lys Ile Ala Gln Leu Leu Arg Asn Lys Val His Ala Val Asn Ile Thr
 35 40 45

Asp Gly Ser Arg Ala Ile Met Arg Met Cys Ser Leu Ala Met Ser Lys
 50 55 60

Leu Leu Leu Asp Asn Gly Ile Glu Pro Ile Met Gln Ile Ser Cys Arg
 65 70 75 80

Asp Arg Asn Lys Ile Ala Leu Gln Ser Asp Ile Leu Gly Ala Asn Ala
 85 90 95

Gly Ile Lys Asn Ile Leu Cys Ile Thr Gly Asp Ser Val Lys Ala
 100 105 110

Gly Asp Gln Gln Glu Thr Lys Ala Val His Glu Phe Glu Ala Val Arg
 115 120 125

Leu Leu Lys Gln Ile Gln Ser Phe Asn Gln Gly Ile Asp Pro Thr Phe
 130 135 140

Glu Gln Leu Pro Asp Lys Arg Thr Glu Ile Phe Ser Gly Ala Ala Val
 145 150 155 160

Asp Pro Ser Cys Arg Asn Gln Arg Ser Leu Lys Ser Arg Thr Ile Lys
 165 170 175

Lys Lys Glu Ala Gly Ala Asn Phe Leu Gln Thr Gln Ile Val Met Asp
 180 185 190

Arg Lys Cys Leu Ala Asp Phe Cys Asn Glu Ile Ser Asn Pro Leu Glu
 195 200 205

Ile Pro Val Ile Ala Gly Val Phe Leu Leu Lys Ser Tyr Lys Asn Ala
 210 215 220

Leu Phe Ile Asn Lys Phe Val Pro Gly Ala Asn Ile Pro Glu Asn Val
 225 230 235 240

Leu Asn Arg Leu Lys Asp Ala Lys Asn Pro Leu Gln Glu Gly Ile Leu
 245 250 255

Ile Ala Ser Glu Gln Ala Gln Asp Phe Ile Asn Ile Ala Asp Gly Ile
 260 265 270

His Leu Met Ala Val Lys Ser Glu His Leu Ile Pro Glu Ile Leu Glu
 275 280 285

Lys Ala Gly Leu Asn Leu Glu Cys
 290 295

<210> 53
 <211> 1848
 <212> DNA
 <213> Bacillus stearothermophilus

<220>
 <221> CDS
 <222> (1)..(1845)
 <223> RBE04103

<400> 53
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 Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly
 1 5 10 15

gcg atg gga acg ctt tta tat tcg cac ggc att gac cgt tgt ttt gaa 96
 Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu
 20 25 30

gaa ttg aat cta tcc aat cca gat gaa atc gtc cat att cat gaa gcg 144
 Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala
 35 40 45

atc gcc gcg ggc gcc gac gtc att cag acg aat aca tac ggc gcc 192
 Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala
 50 55 60

aac tat gtg aaa ctc gcc cgc tac ggc ctt gaa gat gag gtg ccg gcc 240
 Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala
 65 70 75 80

atc aac cgc gcg gcg gtg cgg ctc gcc agg caa gcg gcg aac gga cgg 288
 Ile Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg
 85 90 95

gca tac gtg ctc ggg acg atc ggg ggg ctg cgc acg tta aac aaa agc 336
 Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser
 100 105 110

gtc gtc acg ctc gaa gaa gtg aag cgg acg ttt cgc gag cag ctg ttt 384
 Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe
 115 120 125

gtc ctg ctc gct gaa ggg gtc gac ggc gtg ctg ctc gag acg tat tac	432
Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr	
130 135 140	
gat ttg gaa gag ttg gag acg gtg ctt gcc atc gcc cgc aaa gag acc	480
Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr	
145 150 155 160	
gac ttg ccg att atc gct cac gtc tcg ctc cat gaa gtc ggc gtc ttg	528
Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu	
165 170 175	
caa gat ggc acg ccg ctc gcg gac gcc ctt gcc cgc cta gag gcg ctc	576
Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu	
180 185 190	
ggg gcc gat gtc gtc gga ctg aac tgt cgt ctc ggt cca tat cat atg	624
Gly Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met	
195 200 205	
ctt cgg tcg ctc gag gaa gtg ccg ctg cca aat cga gcg ttt ttg tcg	672
Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser	
210 215 220	
gcg tat ccg aac gcc agc ctt ccg gat tac cgc gat ggg cgg ctt gtc	720
Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val	
225 230 235 240	
tat gag acg aac gct gaa tat ttc gag gaa acg gcc aaa gcg ttc cgc	768
Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg	
245 250 255	
gac caa ggg gtg cgc ttg atc ggc ggg tgc tgc ggc acg acg ccg aaa	816
Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys	
260 265 270	
cat atc gaa gcg atg gca aaa gcg ctc tcc gac cga acg ccg gtg acg	864
His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr	
275 280 285	
gaa aaa acg gtg aaa cgg cgc gcg gtg tct gta tca gtg caa gcg gag	912
Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu	
290 295 300	
ggg ccc gcc cca tct ccc ctt ccc gag ctt gcc cgc acg cac cgc tcg	960
Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser	
305 310 315 320	
gtc att gtg gag ctg gat ccg ccg aaa aaa ttg ggg att gac aag ttt	1008
Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe	
325 330 335	
ctt gcc ggg gcg aaa gcg ctc cat gac gcc ggc atc gat gcg ctg acg	1056
Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr	
340 345 350	
ttg gcc gac aac tcg ctc gcc acg ccg cgc atc agc aac gcc gct gtc	1104
Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val	
355 360 365	
gcc acg atc atc aag gag caa ctc ggc atc cgc ccg ctc gtg cat att	1152
Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile	
370 375 380	

aca tgc cgc gat cgc aat ttg atc ggc ttg cag tcg cat ttg atg ggc Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly 385 390 395 400	1200
ttg cat acg ctc ggc atc acc gat gtg ctc gcc att acc ggc gac ccg Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro 405 410 415	1248
tcg aaa atc ggc gat ttt cca ggg gca acg tcc gtg tac gac tta tca Ser Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser 420 425 430	1296
tcg ttc gat ttg atc cgc ttg atc cgc cag ttt aac gaa ggg ctg tcg Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser 435 440 445	1344
tac tcg ggc aaa ccg ctt ggg caa aaa acg aac ttc tcg atc ggc gct Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala 450 455 460	1392
gtc ttc aac ccg aac gtc cgc cat ttg gac aaa gcg gtc gag cgg atg Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met 470 475 480	1440
gag aaa aaa atc caa tgc ggc gcc cat tat ttc ttg acc cag ccg att Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile 485 490 495	1488
tac tcg gaa gag aaa atc gtt gaa gtg cac gaa gcg acc aag cat ctt Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu 500 505 510	1536
gac acg ccg att tac atc ggc att atg ccg ctt gtg agc gcg cgc aac Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn 515 520 525	1584
gcc gac ttt ttg cat cat gaa gtg ccg ggc att acg ctc tct gac gag Ala Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu 530 535 540	1632
att cgc gcc cgc atg gcc gcc tgc agc ggc gac ccg gtg caa gca gcc Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala 550 555 560	1680
aag gaa ggc atc gct atc gcc aaa tcg ctc att gac gct gcg ttt gat Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp 565 570 575	1728
ttg ttt aac ggc att tat ttg atc acg ccg ttc ttg cgc tac gac atg Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met 580 585 590	1776
acg gtc gag ctt gtc cgc tac att cac gaa aaa gaa gcg gcc gcc aaa Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys 595 600 605	1824
gaa agg aag gtt gtt cat ggc taa Glu Arg Lys Val Val His Gly 610 615	1848

<211> 615
<212> PRT
<213> Bacillus stearothermophilus

<400> 54

Val Gly Leu Leu Asp Glu Leu Lys Glu Arg Ile Leu Ile Ala Asp Gly
1 5 10 15

Ala Met Gly Thr Leu Leu Tyr Ser His Gly Ile Asp Arg Cys Phe Glu
20 25 30

Glu Leu Asn Leu Ser Asn Pro Asp Glu Ile Val His Ile His Glu Ala
35 40 45

Tyr Ile Ala Ala Gly Ala Asp Val Ile Gln Thr Asn Thr Tyr Gly Ala
50 55 60

Asn Tyr Val Lys Leu Ala Arg Tyr Gly Leu Glu Asp Glu Val Pro Ala
65 70 75 80

Asn Arg Ala Ala Val Arg Leu Ala Arg Gln Ala Ala Asn Gly Arg
85 90 95

Ala Tyr Val Leu Gly Thr Ile Gly Gly Leu Arg Thr Leu Asn Lys Ser
100 105 110

Val Val Thr Leu Glu Glu Val Lys Arg Thr Phe Arg Glu Gln Leu Phe
115 120 125

Val Leu Leu Ala Glu Gly Val Asp Gly Val Leu Leu Glu Thr Tyr Tyr
130 135 140

Asp Leu Glu Glu Leu Glu Thr Val Leu Ala Ile Ala Arg Lys Glu Thr
145 150 155 160

Asp Leu Pro Ile Ile Ala His Val Ser Leu His Glu Val Gly Val Leu
165 170 175

Gln Asp Gly Thr Pro Leu Ala Asp Ala Leu Ala Arg Leu Glu Ala Leu
180 185 190

Ala Asp Val Val Gly Leu Asn Cys Arg Leu Gly Pro Tyr His Met
195 200 205

Leu Arg Ser Leu Glu Glu Val Pro Leu Pro Asn Arg Ala Phe Leu Ser
210 215 220

Ala Tyr Pro Asn Ala Ser Leu Pro Asp Tyr Arg Asp Gly Arg Leu Val
225 230 235 240

Tyr Glu Thr Asn Ala Glu Tyr Phe Glu Glu Thr Ala Lys Ala Phe Arg
245 250 255

Asp Gln Gly Val Arg Leu Ile Gly Gly Cys Cys Gly Thr Thr Pro Lys
260 265 270

His Ile Glu Ala Met Ala Lys Ala Leu Ser Asp Arg Thr Pro Val Thr
275 280 285

Glu Lys Thr Val Lys Arg Arg Ala Val Ser Val Ser Val Gln Ala Glu
290 295 300

Arg Pro Ala Pro Ser Pro Leu Pro Glu Leu Ala Arg Thr His Arg Ser
 305 310 315 320
 Val Ile Val Glu Leu Asp Pro Pro Lys Lys Leu Gly Ile Asp Lys Phe
 325 330 335
 Leu Ala Gly Ala Lys Ala Leu His Asp Ala Gly Ile Asp Ala Leu Thr
 340 345 350
 Leu Ala Asp Asn Ser Leu Ala Thr Pro Arg Ile Ser Asn Ala Ala Val
 355 360 365
 Ala Thr Ile Ile Lys Glu Gln Leu Gly Ile Arg Pro Leu Val His Ile
 370 375 380
 Thr Cys Arg Asp Arg Asn Leu Ile Gly Leu Gln Ser His Leu Met Gly
 385 390 395 400
 Leu His Thr Leu Gly Ile Thr Asp Val Leu Ala Ile Thr Gly Asp Pro
 405 410 415
 Lys Ile Gly Asp Phe Pro Gly Ala Thr Ser Val Tyr Asp Leu Ser
 420 425 430
 Ser Phe Asp Leu Ile Arg Leu Ile Arg Gln Phe Asn Glu Gly Leu Ser
 435 440 445
 Tyr Ser Gly Lys Pro Leu Gly Gln Lys Thr Asn Phe Ser Ile Gly Ala
 450 455 460
 Ala Phe Asn Pro Asn Val Arg His Leu Asp Lys Ala Val Glu Arg Met
 465 470 475 480
 Glu Lys Lys Ile Gln Cys Gly Ala His Tyr Phe Leu Thr Gln Pro Ile
 485 490 495
 Tyr Ser Glu Glu Lys Ile Val Glu Val His Glu Ala Thr Lys His Leu
 500 505 510
 Asp Thr Pro Ile Tyr Ile Gly Ile Met Pro Leu Val Ser Ala Arg Asn
 515 520 525
 Asp Phe Leu His His Glu Val Pro Gly Ile Thr Leu Ser Asp Glu
 530 535 540
 Ile Arg Ala Arg Met Ala Ala Cys Ser Gly Asp Pro Val Gln Ala Ala
 545 550 555 560
 Lys Glu Gly Ile Ala Ile Ala Lys Ser Leu Ile Asp Ala Ala Phe Asp
 565 570 575
 Leu Phe Asn Gly Ile Tyr Leu Ile Thr Pro Phe Leu Arg Tyr Asp Met
 580 585 590
 Thr Val Glu Leu Val Arg Tyr Ile His Glu Lys Glu Ala Ala Ala Lys
 595 600 605
 Glu Arg Lys Val Val His Gly
 610 615

<210> 55

<211> 52

<212> DNA
 <213> Künstliche Sequenz

 <220>
 <223> Beschreibung der künstlichen Sequenz:PCR primer

 <400> 55
 cccgggatcc gctagcggcg cgccggccgg cccggtgtga aataccgcac ag 52

 <210> 56
 <211> 53
 <212> DNA
 <213> Künstliche Sequenz

 <220>
 <223> Beschreibung der künstlichen Sequenz:PCR primer

 <400> 56
 tctagactcg agcggccgcg gccggccttt aaattgaaga cgaaagggcc tcg 53

 > 57
 > 47
 <212> DNA
 <213> Künstliche Sequenz

 <220>
 <223> Beschreibung der künstlichen Sequenz:PCR primer

 <400> 57
 gagatctaga cccgggggatc cgctagcggg ctgctaaagg aagcgga 47

 <210> 58
 <211> 38
 <212> DNA
 <213> Künstliche Sequenz

 <220>
 <223> Beschreibung der künstlichen Sequenz:PCR primer

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<223> Beschreibung der künstlichen Sequenz: Plasmid

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<212> DNA

<213> Künstliche Sequenz

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